Table 42: Comparative Sequences relating to SAG 0764

SEQ ID NO. 4201: 2603 V/R STRAIN
ATGGTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGGAATAAAGCTAACCTTTTC
ACTGGATGGGCTGACGTAGATCTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG
AAATTAATTCAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGT
GCCATCAAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA
AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATAAAGCAGAA
GCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGTCGTTCATATGATGTATTG
CCTCCAGATATGGCTAAAGATGATGAACATTCAGCACATACTGATCGTCGCTATGCTTCA
CTAGATGATTCTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTT
CCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGGT
GCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAGATGATGAA
ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTTGATGAAAAATTA
AACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4202: 090 STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTG
GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTCAGAAA
AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
ATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAC
AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
AATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAAT
AAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCG
TCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATT
CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCA
GATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTCTGGGA
AGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGGTG
CACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCA
GATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
CGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4203: A909 STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTCAGAAAA
AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGTA
TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
ATCATGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
AAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGT
CGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATTC
AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
ATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTCTGGGAA
GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGGTGC
ACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAG
ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTC
GAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4204: H36B STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCTGAG
TGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTCAGA
AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAG
GTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAA
ACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGA
AAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAA
ATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGG
CGTCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACA
TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTC
CAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTCTGG
GAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGG
TGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGT
CAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTT
TTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGGTAA
A

SEQ ID NO. 4205: 18RS21 STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTCAGAAAA
AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGTA
TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
AAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGT
CGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATTC
AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
ATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTCTGGGAA
GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGGTGC
ACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAG
ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTC
GAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4206: M732 STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTCAGAAAA
AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGTA

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
AAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGT
CGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGAACATTC
AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
ATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTCTGGGAA
GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTTGGTGC
ACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAATTGTCAG
ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTC
GAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4207: COH1 STRAIN
GTAAAATTAGTATTCGCACGCCACGG
TGAATCTGAGTGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
ATCTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
TGCCATCAAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
ACAGGAAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGT
TCATATTTGGCGTCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAG
ATGATGAACATTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGAT
TCTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCT
TCCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
TGTTTGTTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATC
AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCC
ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATT
ACTTAGGTAAA

SEQ ID NO. 4208: CJB110 STRAIN
GTAAAATTAGTATTCGCACGCCACGG
TGAATCTGAGTGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
ATCTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
TGCCATCAAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
ACAGGAAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGT
TCATATTTGGCGTCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAG
ATGATGAACATTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGAT
TCTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCT
TCCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
TGTTTGTTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATC
AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCC
ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATT
ACTTAGGTAAA

SEQ ID NO. 4209: 1169NT STRAIN
AGTATTCGCACGCCACGGTGAATCTGAGTGGAATAAAGCTAACCTTTTCA
CTGGATGGGCTGACGTAGATCTTTCAGAAAAAGGTACACAACAAGCTATT
GATGCTGGGAAATTAATTCAAGCAGCAGGTATTGAGTTCGACCTTGCTTT
TACATCAGTTCTTAAACGTGCCATCAAAACAACTAACCTTGCCCTTGAAG
CAGCTGATCAACTTTGGGTACCAGTTGAAAAATCATGGCGCTTGAACGAA
CGTCATTACGGTGGATTGACAGGAAAAAATAAAGCAGAAGCAGCTGAACA
ATTTGGTGATGAGCAAGTTCATATTTGGCGTCGTTCATATGATGTATTGC
CTCCAGATATGGCTAAAGATGATGAACATTCAGCACATACTGATCGTCGC
TATGCTTCACTAGATGATTCTGTTATTCCAGATGCAGAAAACCTAAAAGT
TACTTTAGAGCGTGCTCTTCCTTTCTGGGAAGATAAAATTGCTCCTGCTC
TTAAAGATGGTAAAAATGTGTTTGTTGGTGCACACGGTAACTCAATCCGT
GCTCTTGTAAAACATATCAAACAATTGTCAGATGATGAAATCATGGACGT
TGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTTGATGAAAAATTAA
ACCTTGTTTCAGAATATTACTTAGGTAAA

SEQ ID NO. 4210: M781 STRAIN
GTAAAATTAGTATTCGCACGCCACGGT
GAATCTGAGTGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGA
TCTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTC
AAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGT
GCCATCAAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGT
ACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGA
CAGGAAAAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTT
CATATTTGGCGTCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGA
TGATGAACATTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATT
CTGTTATTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTT
CCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGT
GTTTGTTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCA
AACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCA
CCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTA
CTTAGGTAAA

SEQ ID NO. 4211: JM930013 STRAIN
GTAAAATTAGTATTCGCACGCCACGGTGAATCT
GAGTGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTC
AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAG

Table 42: Comparative Sequences relating to SAG 0764

```
CAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC
AAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGT
TGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAA
AAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATT
TGGCGTCGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGA
ACATTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTA
TTCCAGATGCAGAAAACCTAAAAGTTACTTTAGAGCGTGCTCTTCCTTTC
TGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGT
TGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAACATATCAAACAAT
TGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTT
GTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAATATTACTTAGG
TAAA
```

```
PRETTY of: /biotmp/msa63264.2{*}   March 10, 2003 09:30  ..

                           1                                                  50
      msa63264.2{110_090}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
    msa63264.2{110_1169NT}  ---------- -AGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
    msa63264.2{110_18RS21}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_2603}  atggtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
    msa63264.2{110_CJB110}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_COH1}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_H36B}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
 msa63264.2{110_JM9130013}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_M732}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_M781}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
     msa63264.2{110_A909}  ---gtaaaat tAGTATTCGC ACGCCACGGT GAATCTGAGT GGAATAAAGC
                Consensus  ***------- -********* ********** ********** **********

                           51                                                100
      msa63264.2{110_090}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
    msa63264.2{110_1169NT}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
    msa63264.2{110_18RS21}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_2603}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
    msa63264.2{110_CJB110}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_COH1}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_H36B}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
 msa63264.2{110_JM9130013}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_M732}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_M781}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
     msa63264.2{110_A909}  TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
                Consensus  ********** ********** ********** ********** **********

                           101                                               150
      msa63264.2{110_090}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
    msa63264.2{110_1169NT}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
    msa63264.2{110_18RS21}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_2603}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
    msa63264.2{110_CJB110}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_COH1}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_H36B}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
 msa63264.2{110_JM9130013}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_M732}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_M781}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
     msa63264.2{110_A909}  AACAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
                Consensus  ********** ********** ********** ********** **********

                           151                                               200
      msa63264.2{110_090}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
    msa63264.2{110_1169NT}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
    msa63264.2{110_18RS21}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_2603}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
    msa63264.2{110_CJB110}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_COH1}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_H36B}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
 msa63264.2{110_JM9130013}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_M732}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_M781}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
     msa63264.2{110_A909}  GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
                Consensus  ********** ********** ********** ********** **********

                           201                                               250
      msa63264.2{110_090}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
    msa63264.2{110_1169NT}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
    msa63264.2{110_18RS21}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
     msa63264.2{110_2603}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
    msa63264.2{110_CJB110}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
     msa63264.2{110_COH1}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
     msa63264.2{110_H36B}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
 msa63264.2{110_JM9130013}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
     msa63264.2{110_M732}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
     msa63264.2{110_M781}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
```

Table 42: Comparative Sequences relating to SAG 0764

```
      msa63264.2{110_A909}  TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AATCATGGC
                 Consensus  ********** ********** ********** ********** *********

                            251                                               300
       msa63264.2{110_090}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
    msa63264.2{110_1169NT}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
    msa63264.2{110_18RS21}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_2603}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
    msa63264.2{110_CJB110}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_COH1}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_H36B}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
 msa63264.2{110_JM9130013}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_M732}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_M781}  GCTTgAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
      msa63264.2{110_A909}  GCTTaAACGA ACGTCATTAC GGTGGATTGA CAGGAAAAAA TAAAGCAGAA
                 Consensus  ****_***** ********** ********** ********** **********

                            301                                               350
       msa63264.2{110_090}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
    msa63264.2{110_1169NT}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
    msa63264.2{110_18RS21}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_2603}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
    msa63264.2{110_CJB110}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_COH1}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_H36B}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
 msa63264.2{110_JM9130013}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_M732}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_M781}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
      msa63264.2{110_A909}  GCAGCTGAAC AATTTGGTGA TGAGCAAGTT CATATTTGGC GTCGTTCATA
                 Consensus  ********** ********** ********** ********** **********

                            351                                               400
       msa63264.2{110_090}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
    msa63264.2{110_1169NT}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
    msa63264.2{110_18RS21}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_2603}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
    msa63264.2{110_CJB110}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_COH1}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_H36B}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
 msa63264.2{110_JM9130013}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_M732}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_M781}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
      msa63264.2{110_A909}  TGATGTATTG CCTCCAGATA TGGCTAAAGA TGATGAACAT TCAGCACATA
                 Consensus  ********** ********** ********** ********** **********

                            401                                               450
       msa63264.2{110_090}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
    msa63264.2{110_1169NT}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
    msa63264.2{110_18RS21}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_2603}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
    msa63264.2{110_CJB110}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_COH1}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_H36B}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
 msa63264.2{110_JM9130013}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_M732}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_M781}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
      msa63264.2{110_A909}  CTGATCGTCG CTATGCTTCA CTAGATGATT CTGTTATTCC AGATGCAGAA
                 Consensus  ********** ********** ********** ********** **********

                            451                                               500
       msa63264.2{110_090}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
    msa63264.2{110_1169NT}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
    msa63264.2{110_18RS21}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_2603}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
    msa63264.2{110_CJB110}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_COH1}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_H36B}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
 msa63264.2{110_JM9130013}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_M732}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_M781}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
      msa63264.2{110_A909}  AACCTAAAAG TTACTTTAGA GCGTGCTCTT CCTTTCTGGG AAGATAAAAT
                 Consensus  ********** ********** ********** ********** **********

                            501                                               550
       msa63264.2{110_090}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
    msa63264.2{110_1169NT}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
    msa63264.2{110_18RS21}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
      msa63264.2{110_2603}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
    msa63264.2{110_CJB110}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
      msa63264.2{110_COH1}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
      msa63264.2{110_H36B}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
 msa63264.2{110_JM9130013}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
      msa63264.2{110_M732}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
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Table 42: Comparative Sequences relating to SAG 0764

```
    msa63264.2{110_M781}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
    msa63264.2{110_A909}  TGCTCCTGCT CTTAAAGATG GTAAAAATGT GTTTGTTGGT GCACACGGTA
               Consensus  ********** ********** ********** ********** **********

                          551                                                600
     msa63264.2{110_090}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
  msa63264.2{110_1169NT}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
  msa63264.2{110_18RS21}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_2603}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
  msa63264.2{110_CJB110}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_COH1}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_H36B}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
msa63264.2{110_JM9130013} ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_M732}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_M781}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
    msa63264.2{110_A909}  ACTCAATCCG TGCTCTTGTA AAACATATCA AACAATTGTC AGATGATGAA
               Consensus  ********** ********** ********** ********** **********

                          601                                                650
     msa63264.2{110_090}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
  msa63264.2{110_1169NT}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
  msa63264.2{110_18RS21}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_2603}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
  msa63264.2{110_CJB110}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_COH1}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_H36B}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
msa63264.2{110_JM9130013} ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_M732}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_M781}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
    msa63264.2{110_A909}  ATCATGGACG TTGAAATTCC TAACTTCCCA CCACTTGTTT TCGAATTTGA
               Consensus  ********** ********** ********** ********** **********

                          651                                     690
     msa63264.2{110_090}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
  msa63264.2{110_1169NT}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
  msa63264.2{110_18RS21}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_2603}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
  msa63264.2{110_CJB110}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_COH1}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_H36B}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
msa63264.2{110_JM9130013} TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_M732}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_M781}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
    msa63264.2{110_A909}  TGAAAAATTA AACCTTGTTT CAGAATATTA CTTAGGTAAA
               Consensus  ********** ********** ********** **********
```

SEQ ID NO. 4212: 2603 V/R STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4213: 090 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4214: A909 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4215: H36B STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4216: 18RS21 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4217: M732 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4218: COH1 STRAIN

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4219: CJB110 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4220: 1169NT STRAIN
VFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRAIKT
TNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
AKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGAHGN
SIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4221: M781 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4222: JM9130013 STRAIN
VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLP
PDMAKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGKNVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

```
PRETTY of: /biotmp/msa70722.2{*}   March 10, 2003 09:33  ..

                              1                                                   50
      msa70722.2{110_090}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
    msa70722.2{110_18RS21}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_2603}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_A909}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
    msa70722.2{110_CJB110}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_COH1}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_H36B}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
 msa70722.2{110_JM9130013}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_M732}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      msa70722.2{110_M781}   vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
    msa70722.2{110_1169NT}   ---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
                 Consensus   ---******* ********** ********** ********** **********

                              51                                                 100
      msa70722.2{110_090}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
    msa70722.2{110_18RS21}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_2603}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_A909}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
    msa70722.2{110_CJB110}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_COH1}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_H36B}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
 msa70722.2{110_JM9130013}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_M732}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
      msa70722.2{110_M781}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
    msa70722.2{110_1169NT}   LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAEA
                 Consensus   ********** ********** ********** ********** **********

                              101                                                150
      msa70722.2{110_090}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
    msa70722.2{110_18RS21}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_2603}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_A909}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
    msa70722.2{110_CJB110}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_COH1}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_H36B}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
 msa70722.2{110_JM9130013}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_M732}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      msa70722.2{110_M781}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
    msa70722.2{110_1169NT}   AEQFGDEQVH IWRRSYDVLP PDMAKDDEHS AHTDRRYASL DDSVIPDAEN
                 Consensus   ********** ********** ********** ********** **********

                              151                                                200
      msa70722.2{110_090}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
    msa70722.2{110_18RS21}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
      msa70722.2{110_2603}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
      msa70722.2{110_A909}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
    msa70722.2{110_CJB110}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
      msa70722.2{110_COH1}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
      msa70722.2{110_H36B}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
 msa70722.2{110_JM9130013}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
      msa70722.2{110_M732}   LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
```

Table 42: Comparative Sequences relating to SAG 0764

```
    msa70722.2{110_M781}  LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
  msa70722.2{110_1169NT}  LKVTLERALP FWEDKIAPAL KDGKNVFVGA HGNSIRALVK HIKQLSDDEI
               Consensus  ********** ********** ********** ********** **********

                          201                         229
     msa70722.2{110_090}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
   msa70722.2{110_18RS21} MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_2603}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_A909}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
   msa70722.2{110_CJB110} MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_COH1}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_H36B}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
msa70722.2{110_JM9130013} MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_M732}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
    msa70722.2{110_M781}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
  msa70722.2{110_1169NT}  MDVEIPNFPP LVFEFDEKLN LVSEYYLGK
               Consensus  ********** ********** *********
```

Table 43: Comparative Sequences relating to SAG0079

SEQ ID NO. 4301: 2603 V/R STRAIN
ATGAATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTACTCAAGCAGCTAAGATC
GTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCT
AATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT
GATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAA
GGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACG
CTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATCCATCATGT
CTTATAGAGCGTTTGAGTGkTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAA
GTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAG
CCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAA
CACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTT
TTTGCAGATGTTGAAAAAGCGTTGCTAGAACTCAAA

SEQ ID NO. 4302: 090 STRAIN (reverse complement)
AATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTACTCA
AGCAGCTAAGATCGTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCG
CGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGG
TGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGA
TATCGCAGAAAAAGGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGC
CTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGT
GGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGA
AACTTTCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACG
TGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGA
ACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGA
AATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4303: 1169NT STRAIN (REVERSE COMPLEMENT)
TGGTAAAGGGACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTTGCGCACATCTCAAC
AGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAG
TTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAAAGAGCG
CTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGATGGGTATCCACGTACTAT
TGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGT
TATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCAA
TCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGA
AGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTCA
TATTGCTCAAGGAGAACCTATTCTTGAACACTATAGTAAGCTTGGCCTTGTTACAGATAT
TGAAGGTAATCAAGAAATAA

SEQ ID NO. 4304: 18RS21 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAACCACGGGTTCGCCTGGTGCTGGTAAAGGTACTCAAGCAGCTAAGATCG
TTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTA
ATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTG
ATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAG
GTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGC
TTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATCCATCATGTC
TTATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAG
TGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGC
CTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAAC
ACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTT
TTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4305: A909 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTACTCAAGCAG
CTAAGATCGTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCG
CAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAAT
TGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCG
CAGAAAAAGGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAG
ATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATC
CATCATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTT
TCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAG
ATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAATCTA
TTCTTGAACACTATCGAAAGCTTGGTCTTGTTACAGATATTGAAGGTAA

SEQ ID NO. 4306: CJB110 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAACCACGGGTTTGCTTGGTGCTGGTAAAGGTACTCAAGCAGCTAA
GATCGTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAAT
GGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGT
TCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGA
AAAAGGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGC
TACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATCCATC
ATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCA
CAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGA
TAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCT
TGAACACTATAG

SEQ ID NO. 4307: COH1 STRAIN (REVERSE COMPLEMENT)
ATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTACTCAAGCAGCTAAGATTGTTG
AAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATC
AAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATG
AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTT
TTTTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCCTTAGATGCTACGCTTG
AAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATCCAACATGCCTTA
TAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGT

Table 43: Comparative Sequences relating to SAG0079

TCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG
AAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACACT
ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTG
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)
CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAA
GTTATATTGATAAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGC
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGATGGATATCCACGTACTA
TTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTG
TTATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCA
ATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAG
AAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTA
ATATTGCTCAAGGAGAATCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATA
TTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGT
ACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATG
TTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGAT
AAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAG
GATGATATCGCAGAAAAAGGTTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCA
CACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATT
AAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACT
GGTGAAACTTTCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTAT
CAACGTGAAGATGATAAGCCTGAAACTGTTAAACGTCGCTTGGACGTTAATATTGCTCAA
GGAGAACCTATTCTTGAACACTATAAAAAGCTTGGTCTTGTTACAGATATTGAAGGTAAT
CA

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)
CTTTTAATTATGGGTTTGCCTGGTGCTGGTAAAGGTACTCAAGCAGCTAAGATTGTTGAA
GAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATGAA
GTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTT
TTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCCTTAGATGCTACGCTTGAA
GAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTGGATCCAACATGCCTTATA
GAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTC
AACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAA
ACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACACTAT
CGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCA
GATGTTGAAAAAGCGTTG

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAATTACGGGTTTGCCTGGTGCTGGTAAAGGTACTCAA
GCAGCTAAGATTGTTGAAGAATTTGGTGTTGCTCACATCTCAACAGGGGATATGTTCCGC
GCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT
GAATTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGAT
ATCGCAGAAAAAGGTTTTTTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCC
TTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTTATTAATATTAAAGTG
GATCCAACATGCCTTATAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAA
ACTTTCCACAAAGTGTTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGT
GAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAA

MSA Alignment Results: Pretty output

```
PRETTY of: /biotmp/msa25038.2{*}   April 17, 2002 08:53  ..
PRETTY of: /biotmp/msa252229.2{*}   January 31, 2003 03:05  ..

                                 1                                                   50
     msa252229.2{114_COH1}   ----atcttt taattatggg tttgcctggt gctggtaaag gtactcaagc
     msa252229.2{114_M732}   ------cttt taattatggg tttgcctggt gctggtaaag gtactcaagc
     msa252229.2{114_M781}   ---Aatcttt taattacggg tttgcctggt gctggtaaag gtactcaagc
     msa252229.2{114_A909}   ---Aatcttt taattatggg tttgcctggt gctggtaaag gtactcaagc
msa252229.2{114_JM9130013}   ---Aatcttt taattatggg tttgcctggt gctggtaaag gtactcaagc
   msa252229.2{114_CJB110}   ---Aatcttt taaccacggg tttgcttggt gctggtaaag gtactcaagc
      msa252229.2{114_090}   ---Aatcttt taattatggg tttgcctggt gctggtaaag gtactcaagc
     msa252229.2{114_2603}   atgAatcttt taattatggg tttgcctggt gctggtaaag gtactcaagc
     msa252229.2{114_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa252229.2{114_18RS21}   ---Aatcttt taaccacggg ttcgcctggt gctggtaaag gtactcaagc
  msa252229.2{114_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~tggtaaag ggactcaagc
                 Consensus   ****------ ---------- ---------- ---------- ----------

                                 51                                                 100
     msa252229.2{114_COH1}   agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
     msa252229.2{114_M732}   agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
     msa252229.2{114_M781}   agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
     msa252229.2{114_A909}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
msa252229.2{114_JM9130013}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
   msa252229.2{114_CJB110}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
      msa252229.2{114_090}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
     msa252229.2{114_2603}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
     msa252229.2{114_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~CAGGGGATA
   msa252229.2{114_18RS21}   agctaagatc gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
   msa252229.2{114_1169NT}   agctaagatt gttgaagaat ttggtgttgc gcacatctca aCAGGGGATA
```

Table 43: Comparative Sequences relating to SAG0079

```
                   Consensus  ---------- ---------- ---------- ---------- -*********

                              101                                                150
    msa252229.2{114_COH1}     TGTTCCGCGC CGCAATGGCT AATCAAACCc AAATGGGACG TTTAGCTAAA
    msa252229.2{114_M732}     TGTTCCGCGC CGCAATGGCT AATCAAACCc AAATGGGACG TTTAGCTAAA
    msa252229.2{114_M781}     TGTTCCGCGC CGCAATGGCT AATCAAACCc AAATGGGACG TTTAGCTAAA
    msa252229.2{114_A909}     TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
msa252229.2{114_JM9130013}    TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
   msa252229.2{114_CJB110}    TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
     msa252229.2{114_090}     TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
    msa252229.2{114_2603}     TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
    msa252229.2{114_H36B}     TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
   msa252229.2{114_18RS21}    TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
   msa252229.2{114_1169NT}    TGTTCCGCGC CGCAATGGCT AATCAAACCg AAATGGGACG TTTAGCTAAA
                   Consensus  ********** ********** *********- ********** **********

                              151                                                200
    msa252229.2{114_COH1}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
    msa252229.2{114_M732}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
    msa252229.2{114_M781}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
    msa252229.2{114_A909}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
msa252229.2{114_JM9130013}    AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
   msa252229.2{114_CJB110}    AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
     msa252229.2{114_090}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
    msa252229.2{114_2603}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
    msa252229.2{114_H36B}     AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
   msa252229.2{114_18RS21}    AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATgAAGTAA CAAACGGGAT
   msa252229.2{114_1169NT}    AGTTATATTG ATAAAGGTGA ATTGGTTCCT GATcAAGTAA CAAACGGGAT
                   Consensus  ********** ********** ********** ***-****** **********

                              201                                                250
    msa252229.2{114_COH1}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
    msa252229.2{114_M732}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
    msa252229.2{114_M781}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
    msa252229.2{114_A909}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
msa252229.2{114_JM9130013}    TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
   msa252229.2{114_CJB110}    TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
     msa252229.2{114_090}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
    msa252229.2{114_2603}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
    msa252229.2{114_H36B}     TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
   msa252229.2{114_18RS21}    TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
   msa252229.2{114_1169NT}    TGTAAAAGAG CGCTTAGCTG AGGATGATAT CGCAGAAAAA GGTTTTTTAC
                   Consensus  ********** ********** ********** ********** **********

                              251                                                300
    msa252229.2{114_COH1}     TTGATGGaTA TCCACGTACT ATTGAgCAAG CACACGCCTT AGATGCTACG
    msa252229.2{114_M732}     TTGATGGaTA TCCACGTACT ATTGAgCAAG CACACGCCTT AGATGCTACG
    msa252229.2{114_M781}     TTGATGGaTA TCCACGTACT ATTGAgCAAG CACACGCCTT AGATGCTACG
    msa252229.2{114_A909}     TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
msa252229.2{114_JM9130013}    TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
   msa252229.2{114_CJB110}    TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
     msa252229.2{114_090}     TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
    msa252229.2{114_2603}     TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
    msa252229.2{114_H36B}     TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
   msa252229.2{114_18RS21}    TTGATGGaTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
   msa252229.2{114_1169NT}    TTGATGGgTA TCCACGTACT ATTGAaCAAG CACACGCCTT AGATGCTACG
                   Consensus  *******-** ********** *****-**** ********** **********

                              301                                                350
    msa252229.2{114_COH1}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
    msa252229.2{114_M732}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
    msa252229.2{114_M781}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
    msa252229.2{114_A909}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
msa252229.2{114_JM9130013}    CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
   msa252229.2{114_CJB110}    CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
     msa252229.2{114_090}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
    msa252229.2{114_2603}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
    msa252229.2{114_H36B}     CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
   msa252229.2{114_18RS21}    CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
   msa252229.2{114_1169NT}    CTTGAAGAAC TAGGACTACG CTTAGATGGT GTTATTAATA TTAAAGTGGA
                   Consensus  ********** ********** ********** ********** **********

                              351                                                400
    msa252229.2{114_COH1}     TCCAaCATGc CTTATAGAGC GTTTGAGTGg cCGTATTATC AATCGTAAAA
    msa252229.2{114_M732}     TCCAaCATGc CTTATAGAGC GTTTGAGTGg cCGTATTATC AATCGTAAAA
    msa252229.2{114_M781}     TCCAaCATGc CTTATAGAGC GTTTGAGTGg cCGTATTATC AATCGTAAAA
    msa252229.2{114_A909}     TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
msa252229.2{114_JM9130013}    TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
   msa252229.2{114_CJB110}    TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
     msa252229.2{114_090}     TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
    msa252229.2{114_2603}     TCCAtCATGt CTTATAGAGC GTTTGAGTGk tCGTATTATC AATCGTAAAA
    msa252229.2{114_H36B}     TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
   msa252229.2{114_18RS21}    TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
```

Table 43: Comparative Sequences relating to SAG0079

```
   msa252229.2{114_1169NT}  TCCAtCATGt CTTATAGAGC GTTTGAGTGg tCGTATTATC AATCGTAAAA
                 Consensus  ****-****- ********** *********- -********* **********

                            401                                              450
     msa252229.2{114_COH1}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
     msa252229.2{114_M732}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
     msa252229.2{114_M781}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
     msa252229.2{114_A909}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
 msa252229.2{114_JM9130013}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
   msa252229.2{114_CJB110}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
      msa252229.2{114_090}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
     msa252229.2{114_2603}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
     msa252229.2{114_H36B}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
   msa252229.2{114_18RS21}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
   msa252229.2{114_1169NT}  CTGGTGAAAC TTTCCACAAA GTGTTCAACC CACCAGTAGA TTATAAAGAA
                 Consensus  ********** ********** ********** ********** **********

                            451                                              500
     msa252229.2{114_COH1}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
     msa252229.2{114_M732}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
     msa252229.2{114_M781}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
     msa252229.2{114_A909}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
 msa252229.2{114_JM9130013}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TtAAACGTCG
   msa252229.2{114_CJB110}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
      msa252229.2{114_090}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
     msa252229.2{114_2603}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
     msa252229.2{114_H36B}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
   msa252229.2{114_18RS21}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
   msa252229.2{114_1169NT}  GAAGATTACT ATCAACGTGA AGATGATAAG CCTGAAACTG TcAAACGTCG
                 Consensus  ********** ********** ********** ********** *-********

                            501                                              550
     msa252229.2{114_COH1}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatcgta
     msa252229.2{114_M732}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatcgta
     msa252229.2{114_M781}  CTTGGACGTT aATATTGCTC AA~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa252229.2{114_A909}  CTTGGACGTT aATATTGCTC AAggagaatc tattcttgaa cactatcgaa
 msa252229.2{114_JM9130013}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactataaaa
   msa252229.2{114_CJB110}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatag~~
      msa252229.2{114_090}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatcgta
     msa252229.2{114_2603}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatcgta
     msa252229.2{114_H36B}  CTTGGACGTT aATATTGCTC AAggagaatc tattcttgaa cactatcgta
   msa252229.2{114_18RS21}  CTTGGACGTT aATATTGCTC AAggagaacc tattcttgaa cactatcgta
   msa252229.2{114_1169NT}  CTTGGACGTT cATATTGCTC AAggagaacc tattcttgaa cactatagta
                 Consensus  ********** -********* **-------- ---------- ----------

                            551                                              600
     msa252229.2{114_COH1}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
     msa252229.2{114_M732}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
     msa252229.2{114_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa252229.2{114_A909}  agcttggtct tgttacagat attgaaggta a~~~~~~~~~ ~~~~~~~~~~
 msa252229.2{114_JM9130013}  agcttggtct tgttacagat attgaaggta atca~~~~~~ ~~~~~~~~~~
   msa252229.2{114_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa252229.2{114_090}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
     msa252229.2{114_2603}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
     msa252229.2{114_H36B}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
   msa252229.2{114_18RS21}  agcttggtct tgttacagat attgaaggta atcaagaaat aacagaagtt
   msa252229.2{114_1169NT}  agcttggcct tgttacagat attgaaggta atcaagaaat aa~~~~~~~~
                 Consensus  ---------- ---------- ---------- ---------- ----------

                            601                                 636
     msa252229.2{114_COH1}  tttgcagatg ttgaaaaagc gttg~~~~~~ ~~~~~~
     msa252229.2{114_M732}  tttgcagatg ttgaaaaagc gttg~~~~~~ ~~~~~~
     msa252229.2{114_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~
     msa252229.2{114_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~
 msa252229.2{114_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~
   msa252229.2{114_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~
      msa252229.2{114_090}  tttgcagatg ttgaaaaagc gttg~~~~~~ ~~~~~~
     msa252229.2{114_2603}  tttgcagatg ttgaaaaagc gttgctagaa ctcaaa
     msa252229.2{114_H36B}  tttgcagatg ttgaaaaagc gttg~~~~~~ ~~~~~~
   msa252229.2{114_18RS21}  tttgcagatg ttgaaaaagc gttg~~~~~~ ~~~~~~
   msa252229.2{114_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~
                 Consensus  ---------- ---------- ----****** ******
```

SEQ ID NO. 4312: 2603 V/R STRAIN

MNLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVP
DEVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
LIERLSXRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILE
HYRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4313: 090 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN
GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPDQVTNGIVKER
LAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRIIN
RKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHYSKLGLVTDI
EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN
NLLTTGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
YRKLGLVTDIEGNQEITEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN
NLLTTGLLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
Y

SEQ ID NO. 4319: COH1 STRAIN
LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTQMGRLAKSYIDKGELVPDE
VTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPTCLI
ERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEHY
RKLGLVTDIEGNQEITEVFADVEKALL

SEQ ID NO. 4320: H36B STRAIN
GDMFRAAMANQTEMGRLAKSYIDKGELVPDEVTNGIVKERLAEDDIAEKGFLLDGYPRTI
EQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRIINRKTGETFHKVFNPPVDYKEE
DYYQREDDKPETVKRRLDVNIAQGESILEHYRKLGLVTDIEGNQEITEVFADVEKAL

SEQ ID NO. 4321: JM9130013 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEH
YKKLGLVTDIEGN

SEQ ID NO. 4322: M732 STRAIN
LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTQMGRLAKSYIDKGELVPDE
VTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPTCLI
ERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPILEHY
RKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN
NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTQMGRLAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPTCL
IERLSGRIINRKTGETFHKVFNPPVDYKEEDYYQREDDKPETVKRRLDVNIAQ

MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa32357.2{*}   April 17, 2002 09:17 ..

```
                            1                                                  50
   msa252352.2{114_18RS21}  ~nllttgspg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
     msa252352.2{114_M781}  ~nllitglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTqMGRLAK
   msa252352.2{114_CJB110}  ~nllttgllg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
      msa252352.2{114_090}  ~nllimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
msa252352.2{114_JM9130013}  ~nllimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
     msa252352.2{114_A909}  ~nllimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
   msa252352.2{114_1169NT}  ~~~~~~~~~~ ~gkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
     msa252352.2{114_2603}  mnllimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTeMGRLAK
     msa252352.2{114_COH1}  --llimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTqMGRLAK
     msa252352.2{114_M732}  --llimglpg agkgtqaaki veefgvahis tGDMFRAAMA NQTqMGRLAK
     msa252352.2{114_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~GDMFRAAMA NQTeMGRLAK
                 Consensus  *--------- ---------- ---------- -********* ***-******

                            51                                                100
   msa252352.2{114_18RS21}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
     msa252352.2{114_M781}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
   msa252352.2{114_CJB110}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
```

Table 43: Comparative Sequences relating to SAG0079

```
     msa252352.2{114_090}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
msa252352.2{114_JM9130013}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
    msa252352.2{114_A909}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
  msa252352.2{114_1169NT}  SYIDKGELVP DqVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
    msa252352.2{114_2603}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
    msa252352.2{114_COH1}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
    msa252352.2{114_M732}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
    msa252352.2{114_H36B}  SYIDKGELVP DeVTNGIVKE RLAEDDIAEK GFLLDGYPRT IEQAHALDAT
                Consensus  ********** *_******** ********** ********** **********

                           101                                              150
  msa252352.2{114_18RS21}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_M781}  LEELGLRLDG VINIKVDPtC LIERLSgRII NRKTGETFHK VFNPPVDYKE
  msa252352.2{114_CJB110}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
     msa252352.2{114_090}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
msa252352.2{114_JM9130013}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_A909}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
  msa252352.2{114_1169NT}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_2603}  LEELGLRLDG VINIKVDPsC LIERLSxRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_COH1}  LEELGLRLDG VINIKVDPtC LIERLSgRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_M732}  LEELGLRLDG VINIKVDPtC LIERLSgRII NRKTGETFHK VFNPPVDYKE
    msa252352.2{114_H36B}  LEELGLRLDG VINIKVDPsC LIERLSgRII NRKTGETFHK VFNPPVDYKE
                Consensus  ********** ********_* ******_*** ********** **********

                           151                                              200
  msa252352.2{114_18RS21}  EDYYQREDDK PETVKRRLDV nIAQgepile hyrklglvtd iegnqeitev
    msa252352.2{114_M781}  EDYYQREDDK PETVKRRLDV nIAQ~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa252352.2{114_CJB110}  EDYYQREDDK PETVKRRLDV nIAQgepile hy~~~~~~~~ ~~~~~~~~~~
     msa252352.2{114_090}  EDYYQREDDK PETVKRRLDV nIAQgepile hyrklglvtd iegnqeitev
msa252352.2{114_JM9130013}  EDYYQREDDK PETVKRRLDV nIAQgepile hykklglvtd iegn~~~~~~
    msa252352.2{114_A909}  EDYYQREDDK PETVKRRLDV nIAQgesile hyrklglvtd ieg~~~~~~~
  msa252352.2{114_1169NT}  EDYYQREDDK PETVKRRLDV hIAQgepile hysklglvtd iegnqei~~~
    msa252352.2{114_2603}  EDYYQREDDK PETVKRRLDV nIAQgepile hyrklglvtd iegnqeitev
    msa252352.2{114_COH1}  EDYYQREDDK PETVKRRLDV nIAQgepile hyrklglvtd iegnqeitev
    msa252352.2{114_M732}  EDYYQREDDK PETVKRRLDV nIAQgepile hyrklglvtd iegnqeitev
    msa252352.2{114_H36B}  EDYYQREDDK PETVKRRLDV nIAQgesile hyrklglvtd iegnqeitev
                Consensus  ********** ********** _***______ __________ __________

                           201        212
  msa252352.2{114_18RS21}  fadvekalle ~~
    msa252352.2{114_M781}  ~~~~~~~~~~ ~~
  msa252352.2{114_CJB110}  ~~~~~~~~~~ ~~
     msa252352.2{114_090}  fadvekalle LK
msa252352.2{114_JM9130013}  ~~~~~~~~~~ ~~
    msa252352.2{114_A909}  ~~~~~~~~~~ ~~
  msa252352.2{114_1169NT}  ~~~~~~~~~~ ~~
    msa252352.2{114_2603}  fadvekalle LK
    msa252352.2{114_COH1}  fadvekall~ ~~
    msa252352.2{114_M732}  fadvekalle LK
    msa252352.2{114_H36B}  fadvekal~~ ~~
                Consensus  __________ **
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401
STRAIN 2603
GTGGATAAACATCACTCAAAAAAGGCTATTTTAAAGTTAACA
CTTATAACAACTAGTATTTTATTAATGCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA
TTAAAAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCG
GTAACTACTAATACTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG
AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAGAG
TTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAGAATATCCCTCT
AAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCAACTGCAATA
GCACAGAAAGTTCCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT
GTTCTTGATACATCTAAAATAACAAAATTACAAGCCATAACCCAAAGAGGAAAGGGAAAT
GTAGTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGC
CCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAATTTGAGGAATTAAAAGCAAAA
CATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTTTTTGCACATAACTACGCC
AACAATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAAGATGGTTATGGTTCAGAA
GCAAAGAATATTTCGCATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGT
CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAATG
CGTATTCCAGATAAAATTGATTCGGACAAATTTGGTGAAGCATATGCTAAAGCAATCACA
GACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAGTATTGGAAAAACAGCTGATTCT
TTAATTGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTT
GCAGTTGTTGTGGCTGCCGGAAATGAAGGCGCATTTGGTATGGATTATAGCAAACCATTA
TCAACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGAGT
GTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAACTATTGAAGGT
AAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTTGACAAAGGTAAGGCCTACGAT
GTGGTTTATGCCAATTATGGTGCAAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAG
ATTGCATTAATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACA
AATGCAGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTTCTA
ATTCCTTACCGTGAATtACCTGTGGGGATTATTAGTAAAGTAGATGGCGAGCGTATAAAA
AATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTGAAGTAGTTGATAGCCAAGGTGGT
AATCGTATGCTGGAACAATCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGAT
GTAACAGCTTCTGGCTTTGAAATTTATTCTTCAACCTATAATAATCAATACCAAACAATG
TCTGGTACAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCAT
TTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAATTGTCTAAA
AACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAGGATAAGGCGTTTTATTCA
CCACGTCAGCAAGGTGCAGGTGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTAT
ATTACTGGAAACGATGGCAAAGCTAAAATTAATCTCAAACGAATGGGAGATAAATTTGAT
ATCACAGTTACAATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAAT
GTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTAAACCACAAGCCTTGCTAGAT
ACTAATTGGCAGAAAGTAATTCTTCGTGATAAAGAAACACAAGTTCGATTTACTATTGAT
GCTAGTCAATTTAGTCAGAAATTAAAAGAACAGATGGCAAATGGTTATTTCTTAGAAGGT
TTTGTACGTTTTAAAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTA
GGATTTAATGGTGATTTTGCGAACTTACAAGCACTTGAAACACCGATTTATAAGACGCTT
TCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAAGACCAATTGGAGTAC
AATGAATCAGCTCCTTTTGAAAGCAACAACTATACTGCCTTGTTAACACAATCAGCGTCT
TGGGGCTATGTTGATTATGTCAAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCA
AAAAGAATTATTTTAGGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTG
GAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATAGG
GACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTGCTCAAGTT
CTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGTTTTACCATCTTATCGTAAAAAT
TTCCATAATAATCCAAAGCAAAGTGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGT
GGTTTAGATAAGGATGGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTAC
ACACCAGTAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTACT
AAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTAATCGAACATTAAGCTTA
GCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATCGTTTACAATTAGTTTTATCTCAT
GTTGTAAAAGATGAAGAATATGGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA
GAAGGTAAAGTGACACTTCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGAC
CCTAAGGCCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGCAACGGTAAAATTG
TCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAATTTCTAAC
AGTTTCAAATATTTTGATAACTTGAAAAAAGAACCTATGTTTATTTCTAAAAAAGAAAAA
GTAGTAAACAAGAATCTAGAAGAAATAATATTAGTTAAGCCGCAAACTACAGTTACTACT
CAATCATTGTCTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAAC
AATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAAC
CATACCTTACCTAGTACATCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCA
TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAAAGACTAAAAATAATAGTAAA

SEQ ID NO. 4402
STRAIN 090
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGTAATTGCT
AATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATATTGTTGAAAA
AACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAAATGGGTG
ATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAGAGTTA
TCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAGAATA
TCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA
ATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAGAGGTG
AAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAAATAAC
AAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGCTATTA
TTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGCCCA
AAAGATGATAAGCACAGCTTTAAAACTAAAGCAGAATTCGAGGAATTAAA
AGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTTT
TTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGATATTGCAGCA
GCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTCGCATGGTAC
ACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAATCAATG
GTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAATGCGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATGCTAAAGC
AATCACAGACGCTGtTAATCTAGGAGCAAAAaCGATTAATATGAGCCTTG
GAAAAACAGCAGATTCTTTAAttGCaCTCAATGATAAAGTTAAATTAGCA
CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGAAA
TGAAGGTGCATTTGGTATGGATTATAGCAAACCATTATCAACTAATcCTG
ACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTtTGAGTGTT
GCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAACTAT
TGaaGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA
AAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAaAAAAAGAC
TTTGAAGGTAAgGACTTTAAAGGTAAGATTGCATTAATtGAGCGTGGtGG
TGGACTTGATTTTATGACTAAaatCACTcATGCTACAAATGCAgGTGTTG
tTGGTaTCGTtATTtttAACgAtCAAGAaaAACGtGGAAATTTTcTAATT
CCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGGCGAGCG
TATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTgAAGTAG
TTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGGGGCGTG
ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAAT
TTATTCTTCAACCTATAATAATCAATACCAAACAATGTCTGGTACAAGTA
TGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCATTTG
GCTGAGAAATATAAAGGGATGAATTTAgATTCTAAAAAATTGCTAGAATT
GTCTAaAAACATCCTCATGAGCTCAGCaaCAGCATTATATAGTgAAGAgG
ATAAGGCGTtTtATTCaCCACGTCAGCAAGGtGCAGGtGTAGTTGATGCT
GAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAGC
TAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGTTACAA
TTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGTA
GCAACAGAACaAGTAAATAAAGGTAAATTTGCCCTTAAACCACAAGCCtT
GCTAGATACTAATTGGCAGAaAGTAATTCTTcGTGATAAAGAAACACAAG
TTcGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAAAGAACAG
ATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTAAAGAAGCCAA
GGATAGtAATCAGGAGTTAaTGAGTATTCCTTtTGTAGGATttAATGGTG
ATTTTGCGAACTTACAAGCACTTGAAACACCGATTTATAAGACGCTTTCT
AAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAAGACCAATT
GGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATACTGCCTTGT
TAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATGGTGGG
GAGTTAGAATTAGCACCGGAgAGTcCAAAAAGAATTATTTTAgGAACTTT
TGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGATGCAG
CgAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATAGGGAT
GAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTGC
TCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGTTTTAC
CATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCAT
TATCGTATGGATGCCTTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAGT
TGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGTAGCAG
AAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG
TCACCAAATCTTCCTTTACTAGCTCAGTTTGATGAAACTAATCGAACATT
AAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATCGTTTAC
AATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATGAGACT
TCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCCTAA
AACGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGACCCTAAGGCCTTGA
CACTTGTTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAATTGTCT
GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAAT
TTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAAGAATCTATGTTTA
TTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATAACATTA
GTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAAATAAC
TAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAGTAGCA
GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT
ACC

SEQ ID NO. 4403
STRAIN A909
GAGGAGCAAGAATTAAAAAACCAAGAGCAAT
CACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACT
AATACTGTTGAAAAAACATCTGTAACATCTGCTTCTGCTAGTAATACAGC
GAAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT
TATTAGAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGAT
CTTGAAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAG
CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAG
CATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGAT
ACATCTAAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAA
TGTAGTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTC
GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTAaAACTAAGGCAGAA
TTTGAGGAATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAA
CGATAAGATTGtTTTTGCACATAACTACGCCAaCAATACAGAAACGGTGG
CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAAT
ATTTCGCATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACG
TCCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAG
TCTTATTAATGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGTGAA
GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGAT
TAATATGAGCCTTGGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATA
AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTT
GTGGCTGCCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCATT
ATCAACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAG
ATACTTTGAGTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTC
GTTGAAACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTC
TAAACCTTTtTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GTGCAAAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT
AATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA
CAAATGCAGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGT
GGAAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAA
AGTAGATGGCGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACC
AGAGTTTTGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAA
TCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGC
TTCTGGCTTTGAAATTTATTCTTCAACCTATAATAATCAATACCAAACAA
TGTCTGGTACAAGTATGGCTTCACCACATGtTGCAGGATTAATGACAATG
CTTCAAAGTCATTTGGCTGAGaAATATAAAGGGATGAATTTAGATTCTAA
AAAATTGCTAGaATTGTCTAAAAACATcCTCATGAGCTCAGCAACAGCAT
TATATAGTGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCA
GGTGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGG
AAACGATGGCAAAGCTAAAATTAATCTCAAACGAGTGGGAGATAAATTTG
ATATCACAGTTACAATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTAT
TATCAAGCTAATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCT
TaAACCaCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTG
ATAAAGAAACACAAGTTCGATTTACTAtTGATTCTAGTCAATTTAGTCAG
AAATTAAAAGAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACG
TTTTAAAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTG
TAGGATTTAATGGTGATTTTGCGAACTTACAAGCACTTGAAACACCGATT
TATAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAAC
TCATAAAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACA
ACTATACTGCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTAT
GTCAAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAT
TATTTTAGGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTT
TGGAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAA
GATGGAAATAGGGATGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGT
TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGC
AAAGTAAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAG
CAAAGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGA
TAAGGATGGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGTTTACGTT
ACACACCAGTAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTT
CAAGTAAGTACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGA
AACTAATCGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTC
CTACATATCGTCTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAA
TATGGAGATGAGACTTCTTACCATTATTTCCATATAGATCGAGAAGGTAA
AGTGACACTTCCTAAAACAGTTAAGATAGGAGAGAGTGAGGTTGCAGTAG
ACCCTAAGACCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGCA
ACGGTAAAATTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGA
AAACGCTATAGTAATTTCTAACAATTTCAAATATTTTGATAACTTGAAAA
AAGAACCTATGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTA
GAAGAAATAGCATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATT
GTCTAAAGAAATAACTCAATCAGGAAATGAGAAAGTCCTCACTTCTACAA
ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG
GATTCTGTTAACCATACC

SEQ ID NO. 4404
STRAIN H36B
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGTAATTGC
TAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTTGAAA
AAACATCTGTAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT
GATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAGAGTT
ATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAGAAT
ATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACA
AATGCTTCAACTGCAATAGCACAGAAaGTTCCCTCAGCATATGAAGAGGT
GAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGATACATCTAAAATAA
CAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGCTATT
ATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGCCC
AAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAATTTGAGGAATTAA
AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTT
TTTGCACATAACTACGCCAaCAATACAGAAACGGTGGCTGATATTGCAGC
AGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTCGCATGGTA
CACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAATCAAT
GGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAATGCG
TATTCCAGATAAAATTGATTCGGACAAATTTGGTGAAGCATATGCTAAAG
CAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAGCCTT
GGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC
ACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGAA
ATGAAGGTGCATTTGGTATGGATTATAGCAAACCATTATCAACTAATCCT
GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGAGTGT
TGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAACTA
TTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTtTGAC
AAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAAAAGA
CTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCGTGGTG
GTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAGGTGTT
GTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTTCTAAT
TCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGGCGAGC
GTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTGAAGTA
GTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGGGGCGT
GACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAA
TTTATTCTTCAACCTATAATAATCAATACCAAACAATGTCTGGTACAAGT
ATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCATTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT
TGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG
GATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGTAGTTGATGC
TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAG
CTAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGTTACA
ATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT
AGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTAAACCaCAAGCCT
TGCTAGATACTAATTGGCAGAAAGTAATTCTTCGTGATAAAGAAACACAA
GTTCGATTTACTATTGATTCTAGTCAATTTAGTCAGAAATTAAAAGAACA
GATGGCAAATGGTTATTTCTTAGAAGGTTTTGtACGTTTTAAAGAAGCCA
AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTAATGGT
GATTTTGCGAACTtACAAGCACTTGAAACACCGATTTATAAGACGCTTTC
TAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAAGACCAAT
TGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATACTGCCTTG
TTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATGGTGG
GGAGTTAgAATTAgCACCGGAGAGTCCAAAAAGAATTATTTTAGGAACTT
TTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGATGCA
GCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATAGGGA
TGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTG
CTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGTTTTA
CCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCA
TTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAG
TTGTAGCAGATGGTTTTTATACTTATCGTTTACGTTACACACCAGTAGCA
GAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA
GTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTAATCGAACAT
TAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATCGTCTA
CAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGAGATGAGAC
TTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCCTA
AAACAGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGACCCTAAGACCTTG
ACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGCAACGGTAAAATTGTC
TGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAA
TTTCTAACAATTTCAAATATTTTGATAACTTGAAAAAAGAACCTATGTTT
ATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATAGCATT
AGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAAATAA
CTCAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAGTAGC
AGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCA
TACC

SEQ ID NO. 4405
STRAIN 18RS21
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACC
TGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATA
CTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCGAAA
GAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATT
AGAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTG
AAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT
GTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATA
TGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACAT
CTAAAATAACAAAATTACAAGCCATAACCCAAAGAGGAAAGGGAAATGTA
GTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTT
AGATAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAATTTG
AGGAATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGAT
AAGATTGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGA
TATTGCAGCAGCTATGAAAGATGGTTATGGTTCAGAAGCAAAGAATATTT
CGCATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCA
GCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTT
ATTAATGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGTGAAGCAT
ATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAT
ATGAGTATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAAAGT
TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGG
CTGCCGGAAATGAAGGCGCATTTGGTATGGATTATAGCAAACCATTATCA
ACTAATCcTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC
TTTGAGTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTG
AAACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAA
CCTTTTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGC
AAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTG
AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAAT
GCAGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAA
TTTTCTAATTCCTTACCGTGAATTACCTGTGGGGATTATTAgTAAAGTAG
ATGGCGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTtAACCAgAGT
TTTGAAGtAGTTGATAGCCAAGGTGGtAATCGTaTGCTGGAACAATCAAG
TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG
GCTTTGAAATTTATTCTTCAACCTATAATAATCAATACCAAaCAATGTCT
GGTACAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCA
AAGTCATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAAT
TGCTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT
AGTGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGT
AGTTGATGCTGAAAAAGCTATCCAAGCTCaATATTATATTACTGGAAACG
ATGGCAaAGCTAAAATTAATCTCAAACGAATGGGAGATAAATTTGATATC
ACAGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCA
AGCTAATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTaAAC
CACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAA
GAAACACAAGTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA
AAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA
TTTAATGGTGATTTTGCGAACTTACAAGCACTTGAAACACCGATTTATAA
GACGATTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATA
AAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTAT
ACTGCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA
AAATGGTGGGGAGTTAGAATTAGCaCCGGAGAGTCCAAAAAGAATTATTT
TAGGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAA
AGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGG
AAATAGGGACGAAATCACTCCCCAGGCAACtTTCTTAAGAAATGTTAAGG
ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT
AAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAG
TGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGG
ATGGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACA
CCAGTAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTACAAGT
AAGTACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTA
ATCGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACA
TATCGTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGG
GGATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGA
CACTTCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCT
AAGGCCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGcAACGGT
AAAATTGTCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACG
CTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAAGAA
CCTATGTTTATTTCTAAAAAAGAAAAAGTAGTAAACAAGAATCTAGAAGA
AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTA
AAGAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAAT
AATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTC
TGTTAACCATACC

SEQ ID NO. 4406
STRAIN M732
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCT
GTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATAT
TGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAG
AAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTA
GAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGA
AGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATG
TAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATAT
GAAGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATC
TAAAATAACAAAATTACAAGCCACAACCCAAAGAGGAAAGGGAAATGTAG
TAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTA
GATAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAATTTGA
GGAATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATA
AGATTGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGAT
ATTGCAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTT
GCATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAG
CAATCAATAGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTA
TTAATGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATA
TGCTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATA
TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT
AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGC
TGCCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCATTATCAA
CTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACT
TTGAGTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGA
AACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAAC
CTTtTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCA
AAAAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAG
CGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGC
AGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATT
TTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGAT
GGCGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTT
TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTT
GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGC
TTTGAAATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGG
TACAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAA
GTCATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTG
CTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAG
TGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGTAG
TTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGAT
GGCAAAGTTAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCAC
AGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAG
CTAATGTAGCAACAGAaCAAGTAAATAAAGGTAAATTTGCCCTTaAACCA
CAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTCGTGATAAAGA
AACACAAGTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAA
AAGAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTAAA
GAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATT
TAATGGTGATTTTGCGAACTTACAAGCACTTGAAACaCCGATTTATAAGA
CGCTTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAA
GACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATAC
TGCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAA
ATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTA
GGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAG
AGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGAT
ATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAA
GGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTG
ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT
GGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACC
AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAA
GTACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTAAT
CGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATA
TCGTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG
ATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACA
CTTCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAA
GGCCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAA
AATTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGaAAACGCT
ATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACC
TATGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAA
TAACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTGTCTAAA
GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAA
TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG
TTAACCATACC

SEQ ID NO. 4407
STRAIN COH1
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGT
AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTaACTACTAATATTG
TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
ATGGGtgATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGA
AGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAG
AAGAATATCCCTCTAAACCAGAGaCAACCAACAATAAAGAAAGCAATGTA
GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTA
AAATAACAAAATTACAAGCCACAACCCAAAGAGGAAAGGGAAATGTAGTA
GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGA
TAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAATTTGAGG
AAtTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAG
ATTGTTTTTGCACATAACTACGCCAaCAATACAGAAACGGTGGCTGATAT
TGCAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTTGC
ATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCA
ATCAATAGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT
AATGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATG
CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG
AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA
ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTG
CCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCATTATCAACT
AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
GAGTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAA
CAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCT
TtTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA
AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG
TGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAG
GTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTT
CTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGG
CGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTG
AAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG
GGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
TGAaATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
CAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGT
CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAaAAAATTGCT
AGaATTGTCTAaaAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG
AAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGTAGTT
GATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGG
CAAAGTTAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCACAG
TTACAATTCATaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCT
AATGTAGCAaCAGAACAAGTAAATAAAGGTAAATTTGCCCTTAAACCACA
AGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAAGAAA
CACAAGTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAAA
GAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTAAAGA
AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
ATGGTGATTTTGCGAACTTACAAGCACTTGAAACACCGATTTATAAGACG
CTTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAAGA
CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATACTG
CCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT
GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGG
aACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAG
ATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAAT
AGGGACGAAATCACTCCCCAGGCaACTTTCTTAAGAAATGTTAAGGATAT
TTCTGCTCAAGtTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGG
TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAAGTGAT
GGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAgATAAGGATGG
CAAAGTTGTAgCAGATGGtTTTTATACTTATCGCTTACGTTACACACCAG
TAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTaAAGTTCAAGTAAGT
AcTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGaAACTAATCG
AACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATC
GTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
TCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGG
CCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCTA
TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATA
ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTGTCTAAAGA
AATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATA
GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT
AACCATACC

SEQ ID NO. 4408
STRAIN M781
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGT
AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATATTG
TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
ATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGA
AGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAG
AAGAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTA
GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTA
AAATAACAAAATTACAAGCCACAACCCAAAGAGGAAAGGGAAATGTAGTA
GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGA
TAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAATTTGAGG
AATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAG
ATTGTTTTTGCACATAACTACGCCAaCAATACAGAAACGGTGGCTGATAT
TGCAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTTGC
ATGGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCA
ATCAATAGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT
AATGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATG
CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG
AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA
ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTG
CCGGAAATGAAGGTGCATTTGGTATGGATTATAGCAAaCCATTATCAaCT
AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
GAGTGTTGCTAGCTATGAATCACTtAAAACTATCAGTGAGGTCGTTGAAA
CAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACtTCTAaACCT
TTTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA
AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG
TGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAG
GTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTT
cTAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGG
CGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTg
AAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG
GGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
TGAAATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
CAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGT
CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCT
AGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG
AAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGTAGTT
GATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGG
CAAAGTTAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCACAG
TTACAATTCATaaACTTGTAgAAGGTGTCAAAGAATTGTATTATCAAGCT
AATGTAGCaaCAGAACAAGTAAATAaAGGTAAATTTGCCCTTaAaCCaCA
AGCCTTGCTAGATACTAATTGGCAGAaAGTaATTCTTcGTGATAAAGAAA
CACAAGTTcGATTTACTAtTGATGCTAGTCAATTTAGTCAGAAATTAAAA
GAACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTAAAGA
AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
ATGGTGATTTTGCGAACTtACAAGCACTTGAAACACCGATTTATAAGACG
CTTTCTAAAGGTAGTTTCTACTATAAaCCAAATGATACAACTCATAAAGA
CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATACTG
CCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT
GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGG
AACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAG
ATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAAT
AGGGACGaaATCACTCCCCAGGCaACtTTCTTAAGAAATGTTAAGGATAT
TTCTGCTCAAGtTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGG
TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAAGTGAT
GGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGATGG
CAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACCAG
TAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGT
ACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTAATCG
AACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACAtATC
GTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGAT
GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
TCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGG
CCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCTA
TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATA
ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTGTCTAAAGA
AATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATA
GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409
STRAIN CJB110
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGTAA
TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATATTGTT
GAAAAAACATCTGTAnCAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG
AGTTATCTAAAAACCTTGATACGTCTAATwTGGGGGCTGATCTTGAAGAA
GAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGT
AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAG
AGGTGaAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA
ATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGC
TATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATA
GCCCAAAAGATGATAAGCACAGCTTTAAAACTAAAGCAGAATTCGAGGAA
tTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT
TGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGATATTG
CAGCAGCTATGAAAGATGGTTATGGGTCAGAAGCAAAGAATATTTCGCAT
GGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAAT
CAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAA
TGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATGCT
AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAG
CCTTGGAAAAACAGCAGATTCTTTAATTGCACTCAATGATAAAGTTAAAT
TAgCACTTAAATTAGCTTcTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCC
GGAAATGAAGGTGCATTTGGTATGGATTATAgCAAACCATTATCAACTAA
TcCTGACTACGGtACGGTTAATAGTCCAGCTATTTcTGAAGATACTTTGA
GTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGaAACA
ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTcTAAACCTTT
TGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCGT
GGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAGG
TGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTTc
TAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGGC
GAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAgAGTTTTGA
AGTAgTTGATAGCCAAgGTGGCAATCGTATGCTGGAACAATCAAGTtGGG
GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT
GAAATTTATTCTTCAACCTATAATAATCAATACCAAACAATGTCTGGTAC
AAGTATGGCTTCACCACATGtTGCAGGATTAATGACAATGCTTCAAAATC
ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA
GAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
AGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGtGCAGGTGTAGTTG
ATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGC
AAAGCTAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGT
TACAATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTA
ATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTaAACCACAA
GCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAAGAAAC
ACAAGTTCGATTTACTAtTGATGCTAGTCAATTTAgTCAGAAATTAAAAG
AACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTAAAGAA
GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTAA
TGGTGATTTTGCGAACTtACAAGCACTTGAAACACCGATTTATAAGACGC
TTTCTAAAGGTAGTtTCTACTATAAACCAAATGATACAACTCATAAAGAC
CAATTGGAGTACAATGAATCAGCTCctTTTGAAAGCAACAACTATACTGC
CTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG
GTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGGA
ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGA
TGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATA
GGGATGaaATCACTCCCCAGGCAACtTTCTTAAGAAATGTTAAGGATATT
TCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGT
TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG
GTCATTATCGTATGGATGCCTTTCAGTGGAGTGGTTTAgATAAgGATGGC
AAAGTTGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGT
AGCAGAAgGAGCAAATAGTCAGGAGTCAgACTTTAAAGTTCAAGTAAGTA
CTAAGTCACCAAATCTTCCTTTACTAGCTCAGTTTGATGAAACTAATCGA
ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATCG
TTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG
AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTT
CCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGACCCTAAGGC
CTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTaAAAT
TGTCTGACCTCTTGAaTAAgGCAGTAGTATCAGAGAAAGAAAACGCTATA
GTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAAGAATCTAT
GTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATAA
CATTAGTTAAGCCGCAaACTACAGTTACTACTCAATCATTGTCTAAAGAA
ATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAG
TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
ACCATACC

SEQ ID NO. 4410
STRAIN 1169NT
GAGGAGCAAGAATTAAAAAACCAAGAGCAATC
ACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTA
ATATTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG
AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATT
ATTAGAAGAGTTATCTAAAAACCTTGATACGTCTAATATGGGGGCTGATC

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

TTGAAGAAGAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC
AATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC
ATATGAAGAGGTGAAGCCAAAAAGCAAGTCATCGCTTGCTGTTCTTGATA
CATCTAAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAAT
GTAGTAGCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCG
TTTAGATAGCCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAT
TCGAGGAATTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAAC
GATAAGATTGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGC
TGATATTGCAGCAGCTATGAAAgATGGTTATGGTTCAGAAGCAAAGAATA
TTTCGCATGGTACACACGTTGCTGGTATTtTTGTAGGTAATAGTAAACGT
CCAGCAATCAATGGTCTTCTTTTAgAAGGTGCAgCGCCAAATGCTCAAGT
CTTATTAATGCGTATTCCAGATAAAATtGATTCGGACAAATTtGGAGAAG
CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTaAAACGATT
AATATGAGTATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAA
AGTTAAATTAgCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTG
TGGCTGcCGGAAATGAAGGCGCATTtGGTATGGATTATAGCAAACCGTTA
TCAACTAATcCTGACTACGGtACGGtTAATAGTCCAGCTATTTCTGAAGA
TACTTTGAGTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCG
TTGAAACAACTATTGAAGGTAAGTTAGTTAAGTtGCCGATTGtGACTTCT
AAACCTTttGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGG
TGCAAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAA
TTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACA
AATGCAGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGG
AAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAG
TAGATGGCGAGCGTATAAAAaATACTTCAAGTCAGTTAACATTTAACCAg
AGATTTGAAGTAGTTGATAGCCAAgGTGGCAATCGTATGCTGGAACAATC
aAGTtGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTT
CTGGCTTCGaAATTTATTCTTCaaCCTATAATAATCAATACCAAACAATG
TCTGGTACAAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCT
TCAAAGTCATTTGGCTGAGaAATATAAAGGGATGAATTTAgATTCTAaAA
AATTGCTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTA
TATAGTGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGtGCAGG
TGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA
ACGATGGCAAAGCTAAAATTAATCTCAAACGAGTGGGAGATAAATTTGAT
ATCACAGTTACAATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTA
TCAAGCTAATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTA
AACCACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGAT
AAAGAAACACAAGTTCGATTTACTATTGATGCTAGTCAATTTAgTCAGAA
ATTAAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTT
TTAAAGAAGCTAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTA
GGATTTAATGGTGATTTTGCGAGCTTACAAGCACTTGAAACACCGATTTA
TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTC
ATAAAGACCAATTGGAGTATAATGAATCAGCTCCTTTTGAAAGCAACAAC
TATACTGCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGT
CaAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTA
TTTTAGGAACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTG
GAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGA
TGGAAATAGGGATGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTA
AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAA
AGTAAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCA
GAGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAgATA
AGGATGGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTAC
ACACCAGTAGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCA
AGTAAGTACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGaAA
CTAATCGAACATTAAGCTTAGCCATGCCTAAGGGAAGTAGTTATGTTCCT
ATATATCGTCTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATA
TGGAGATGAGACTTCTTACTATTATTTCCATATAGATCAAGAAGGTAAAG
CGACACTTCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGAC
CCTAAGGCCTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGCAaC
GGTAAAATTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAA
ACGCTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAA
GAACCTATGTTTATTTCTAAAAAAGAAAAAGTAGTAAACAAGAATCTAGA
AGAaATAATATTAGTTAAGCCGCAcACTACAGTTACTACTCAaTCATTGT
CTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAAC
AATAATAGTAGTAGAGTAGCTAAAATCATATCACCTAAACATAATGGGGA
TTCTGTTAACCATACC

SEQ ID NO. 4411
STRAIN JM9130013
GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCTGTAA
TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTT
GAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG
AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAA
GAATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGT
AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG
AGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTAAA
ATAACAAAATTACAAGCCATAACCCAAAGAGGAAAGGGAAATGTAGTAGC
TATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATA
GCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAATTTGAGGAA
TTAAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT
TGTTTTTGCACATAACTACGCCAACAATACAGAAACGGTGGCTGATATTG
CAGCAGCTATGAAAGATGGTTATGGTTCAGAAGCAAAGAATATTTCGCAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

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GGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCCAGCAAT
CAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAA
TGCGTATTCCAGATAAAATTGATTCGGACAAATTTGGTGAAGCATATGCT
AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAG
TATTGGAAAAACAGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAAAT
TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCC
GGAAATGAAGGCGCATTTGGTATGGATTATAGCAAACCATTATCAACTAA
TCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA
GTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACA
ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT
TGACAAAgGTAAgGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCGT
GGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAGG
TGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAAACGTGGAAATTTTC
TAATTCCTTACCGTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGGC
GAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTTGA
AGTAGTTGATAGCCAAGGTGGTAATCGTATGCTGGAACAATCAAGTTGGG
GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT
GAAATTTATTCTTCAACCTATAATAATCAATACCAAACAATGTCTGGTAC
AAGTATGGCTTCACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTC
ATTTGGCTGAGAAATATAAAGGGaTGAATTTAGATTCTAAAAAATTGCTA
GAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
AGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCAGGTGTAGTTG
ATGCTGAAAAAGCTATCCAAGCTCaATATTATATTACTGGAAACGATGGC
AAAGCTAAAATTAATCTCAAACGAATGGGAGATAAATTTGATATCACAGT
TACAATTCATaAACTTGTAGAAGGTGTCAAAGAAtTGTATTATCAAGCTA
ATGTAGCAACAGAACAAGTAAATAAAGGTAAATTTGCCCTTaAACCACAA
GCCTTGCTAGATACTAATTGGCAGAAAGTAATTCTTCGTGATAAAGAAAC
ACAAGTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAAAG
AACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTAAAGAA
GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTAA
TGGTGATTTTGCGAACTTACAAGCACTTGAAACACCGATTTATAAGACGC
TTTCTAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAAGAC
CAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACAACTATACTGC
CTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG
GTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGGA
ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGA
TGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAATA
GGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATT
TCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGTAAGGT
TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG
GTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGATGGC
AAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACCAGT
AGCAGAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTA
CTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGATGAAACTAATCGA
ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCCTACATATCG
TTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG
AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTT
CCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGGC
CTTGACACTTGTTGTGGAAGATAAAGCTGGTAATTTCGCAaCGGTAAAAT
TGTCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATA
GTAATTTCTaACAGTTTCAAATATTTTGATAACTTGAAAAAAGAACCTAT
GTTTATTTCTAAAAAAGAAAAAGTAGTAAACAAGAATCTAGAAGAAATAA
TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAA
ATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAATAG
TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
ACCATACC
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PRETTY of: /biotmp/msa183564.2{*}   May 13, 2003 03:28  ..

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      msa183564.2{147_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa183564.2{147_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa183564.2{147_2603}  gtggataaac atcactcaaa aaaggctatt ttaaagttaa cacttataac
  msa183564.2{147_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa183564.2{147_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa183564.2{147_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa183564.2{147_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus  ********** ********** ********** ********** **********

                            51                                                100
      msa183564.2{147_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
      msa183564.2{147_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
      msa183564.2{147_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
      msa183564.2{147_2603}  aactagtatt ttattaatgc atagcaatca agtgaatgca GAGGAGCAAG
  msa183564.2{147_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
     msa183564.2{147_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
        msa183564.2{147_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
     msa183564.2{147_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
     msa183564.2{147_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
     msa183564.2{147_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
   msa183564.2{147_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ GAGGAGCAAG
                 Consensus  ********** ********** ********** ********** **********

                            101                                               150
     msa183564.2{147_COH1}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
     msa183564.2{147_M732}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
     msa183564.2{147_M781}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
     msa183564.2{147_2603}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
msa183564.2{147_JM9130013}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
   msa183564.2{147_18RS21}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
      msa183564.2{147_090}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
   msa183564.2{147_CJB110}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
     msa183564.2{147_A909}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
     msa183564.2{147_H36B}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
   msa183564.2{147_1169NT}  AATTAAAAAA CCAAGAGCAA TCACCTGTAA TTGCTAATGT TGCTCAACAG
                 Consensus  ********** ********** ********** ********** **********

                            151                                               200
     msa183564.2{147_COH1}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAaCAgC
     msa183564.2{147_M732}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAaCAgC
     msa183564.2{147_M781}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAaCAgC
     msa183564.2{147_2603}  CCATCGCCAT CGGTAACTAC TAATAcTGTT GAAAAAACAT CTGTAaCAgC
msa183564.2{147_JM9130013}  CCATCGCCAT CGGTAACTAC TAATAcTGTT GAAAAAACAT CTGTAaCAgC
   msa183564.2{147_18RS21}  CCATCGCCAT CGGTAACTAC TAATAcTGTT GAAAAAACAT CTGTAaCAgC
      msa183564.2{147_090}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAaCAgC
   msa183564.2{147_CJB110}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAnCAgC
     msa183564.2{147_A909}  CCATCGCCAT CGGTAACTAC TAATAcTGTT GAAAAAACAT CTGTAaCAtC
     msa183564.2{147_H36B}  CCATCGCCAT CGGTAACTAC TAATAcTGTT GAAAAAACAT CTGTAaCAtC
   msa183564.2{147_1169NT}  CCATCGCCAT CGGTAACTAC TAATAtTGTT GAAAAAACAT CTGTAaCAgC
                 Consensus  ********** ********** *****_**** ********** *****_**_*

                            201                                               250
     msa183564.2{147_COH1}  TGCTTCTGCT AGTAATACAG tGAAAGAAAT GGGTGATACA TCTGTAAAAA
     msa183564.2{147_M732}  TGCTTCTGCT AGTAATACAG tGAAAGAAAT GGGTGATACA TCTGTAAAAA
     msa183564.2{147_M781}  TGCTTCTGCT AGTAATACAG tGAAAGAAAT GGGTGATACA TCTGTAAAAA
     msa183564.2{147_2603}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
msa183564.2{147_JM9130013}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
   msa183564.2{147_18RS21}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
      msa183564.2{147_090}  TGCTTCTGCT AGTAATACAG tGAAAGAAAT GGGTGATACA TCTGTAAAAA
   msa183564.2{147_CJB110}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
     msa183564.2{147_A909}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
     msa183564.2{147_H36B}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
   msa183564.2{147_1169NT}  TGCTTCTGCT AGTAATACAG cGAAAGAAAT GGGTGATACA TCTGTAAAAA
                 Consensus  ********** ********** _********* ********** **********

                            251                                               300
     msa183564.2{147_COH1}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
     msa183564.2{147_M732}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
     msa183564.2{147_M781}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
     msa183564.2{147_2603}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
msa183564.2{147_JM9130013}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
   msa183564.2{147_18RS21}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
      msa183564.2{147_090}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
   msa183564.2{147_CJB110}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
     msa183564.2{147_A909}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
     msa183564.2{147_H36B}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
   msa183564.2{147_1169NT}  ATGACAAAAC AGAAGATGAA TTATTAGAAG AGTTATCTAA AAACCTTGAT
                 Consensus  ********** ********** ********** ********** **********

                            301                                               350
     msa183564.2{147_COH1}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
     msa183564.2{147_M732}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
     msa183564.2{147_M781}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
     msa183564.2{147_2603}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
msa183564.2{147_JM9130013}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
   msa183564.2{147_18RS21}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
      msa183564.2{147_090}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
   msa183564.2{147_CJB110}  ACGTCTAATw TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
     msa183564.2{147_A909}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
     msa183564.2{147_H36B}  ACGTCTAATt TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
   msa183564.2{147_1169NT}  ACGTCTAATa TGGGGGCTGA TCTTGAAGAA GAATATCCCT CTAAACCAGA
                 Consensus  *********_ ********** ********** ********** **********

                            351                                               400
     msa183564.2{147_COH1}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
     msa183564.2{147_M732}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
     msa183564.2{147_M781}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
     msa183564.2{147_2603}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
msa183564.2{147_JM9130013}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
   msa183564.2{147_18RS21}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
      msa183564.2{147_090}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
    msa183564.2{147_CJB110}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
      msa183564.2{147_A909}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
      msa183564.2{147_H36B}  GACAACCAAC AATAAaGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
    msa183564.2{147_1169NT}  GACAACCAAC AATAAgGAAA GCAATGTAGT AACAAATGCT TCAACTGCAA
                  Consensus  ********** *****_**** ********** ********** **********

                             401                                              450
      msa183564.2{147_COH1}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGtC AgAAAGCAAG
      msa183564.2{147_M732}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGtC AgAAAGCAAG
      msa183564.2{147_M781}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGtC AgAAAGCAAG
      msa183564.2{147_2603}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AgAAAGCAAG
 msa183564.2{147_JM9130013}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AgAAAGCAAG
    msa183564.2{147_18RS21}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AgAAAGCAAG
       msa183564.2{147_090}  TAGCACAGAA AGTTCCCTCA GCgTATGAAG AGGTGAAGcC AgAAAGCAAG
    msa183564.2{147_CJB110}  TAGCACAGAA AGTTCCCTCA GCgTATGAAG AGGTGAAGcC AgAAAGCAAG
      msa183564.2{147_A909}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AgAAAGCAAG
      msa183564.2{147_H36B}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AgAAAGCAAG
    msa183564.2{147_1169NT}  TAGCACAGAA AGTTCCCTCA GCaTATGAAG AGGTGAAGcC AaAAAGCAAG
                  Consensus  ********** ********** **_******* ********_* *_********

                             451                                              500
      msa183564.2{147_COH1}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAc
      msa183564.2{147_M732}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAc
      msa183564.2{147_M781}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAc
      msa183564.2{147_2603}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAt
 msa183564.2{147_JM9130013}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAt
    msa183564.2{147_18RS21}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TaCAAGCCAt
       msa183564.2{147_090}  TCATCgCTTG CTGTTtTTGA TACATCTAAA ATAACAAAAT TgCAAGCCAt
    msa183564.2{147_CJB110}  TCATCgCTTG CTGTTtTTGA TACATCTAAA ATAACAAAAT TgCAAGCCAt
      msa183564.2{147_A909}  TCATCaCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TgCAAGCCAt
      msa183564.2{147_H36B}  TCATCaCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TgCAAGCCAt
    msa183564.2{147_1169NT}  TCATCgCTTG CTGTTcTTGA TACATCTAAA ATAACAAAAT TgCAAGCCAt
                  Consensus  *****_**** *****_**** ********** ********** *_*******_

                             501                                              550
      msa183564.2{147_COH1}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
      msa183564.2{147_M732}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
      msa183564.2{147_M781}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
      msa183564.2{147_2603}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
 msa183564.2{147_JM9130013}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
    msa183564.2{147_18RS21}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
       msa183564.2{147_090}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
    msa183564.2{147_CJB110}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
      msa183564.2{147_A909}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
      msa183564.2{147_H36B}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
    msa183564.2{147_1169NT}  AACCCAAAGA GGAAAGGGAA ATGTAGTAGC TATTATTGAT ACTGGCTTTG
                  Consensus  ********** ********** ********** ********** **********

                             551                                              600
      msa183564.2{147_COH1}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
      msa183564.2{147_M732}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
      msa183564.2{147_M781}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
      msa183564.2{147_2603}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
 msa183564.2{147_JM9130013}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
    msa183564.2{147_18RS21}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
       msa183564.2{147_090}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
    msa183564.2{147_CJB110}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
      msa183564.2{147_A909}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
      msa183564.2{147_H36B}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
    msa183564.2{147_1169NT}  ATATTAACCA TGATATTTTT CGTTTAGATA GCCCAAAAGA TGATAAGCAC
                  Consensus  ********** ********** ********** ********** **********

                             601                                              650
      msa183564.2{147_COH1}  AGCTTTAAAA cTAAggCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
      msa183564.2{147_M732}  AGCTTTAAAA cTAAggCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
      msa183564.2{147_M781}  AGCTTTAAAA cTAAggCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
      msa183564.2{147_2603}  AGCTTTAAAA cTAAgaCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
 msa183564.2{147_JM9130013}  AGCTTTAAAA cTAAgaCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
    msa183564.2{147_18RS21}  AGCTTTAAAA cTAAgaCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
       msa183564.2{147_090}  AGCTTTAAAA cTAAagCAGA ATTcGAGGAA TTAAAAGCAA AACATAATAT
    msa183564.2{147_CJB110}  AGCTTTAAAA cTAAagCAGA ATTcGAGGAA TTAAAAGCAA AACATAATAT
      msa183564.2{147_A909}  AGCTTTAAAA cTAAggCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
      msa183564.2{147_H36B}  AGCTTTAAAA cTAAggCAGA ATTtGAGGAA TTAAAAGCAA AACATAATAT
    msa183564.2{147_1169NT}  AGCTTTAAAA aTAAggCAGA ATTcGAGGAA TTAAAAGCAA AACATAATAT
                  Consensus  ********** _***__**** ***_****** ********** **********

                             651                                              700
      msa183564.2{147_COH1}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
      msa183564.2{147_M732}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
      msa183564.2{147_M781}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
      msa183564.2{147_2603}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
 msa183564.2{147_JM9130013}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
    msa183564.2{147_18RS21}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
       msa183564.2{147_090}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
    msa183564.2{147_CJB110}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
      msa183564.2{147_A909}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
      msa183564.2{147_H36B}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
    msa183564.2{147_1169NT}  CACTTATGGG AAATGGGTTA ACGATAAGAT TGTTTTTGCA CATAACTACG
                  Consensus  ********** ********** ********** ********** **********

                             701                                                750
      msa183564.2{147_COH1}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
      msa183564.2{147_M732}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
      msa183564.2{147_M781}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
      msa183564.2{147_2603}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
 msa183564.2{147_JM9130013}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
    msa183564.2{147_18RS21}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
       msa183564.2{147_090}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
    msa183564.2{147_CJB110}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
      msa183564.2{147_A909}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
      msa183564.2{147_H36B}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
    msa183564.2{147_1169NT}  CCAACAATAC AGAAACGGTG GCTGATATTG CAGCAGCTAT GAAAGATGGT
                  Consensus  ********** ********** ********** ********** **********

                             751                                                800
      msa183564.2{147_COH1}  TATGGgTCAG AAGCAAAGAA TATTTtGCAT GGTACACACG TTGCTGGTAT
      msa183564.2{147_M732}  TATGGgTCAG AAGCAAAGAA TATTTtGCAT GGTACACACG TTGCTGGTAT
      msa183564.2{147_M781}  TATGGgTCAG AAGCAAAGAA TATTTtGCAT GGTACACACG TTGCTGGTAT
      msa183564.2{147_2603}  TATGGtTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
 msa183564.2{147_JM9130013}  TATGGtTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
    msa183564.2{147_18RS21}  TATGGtTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
       msa183564.2{147_090}  TATGGgTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
    msa183564.2{147_CJB110}  TATGGgTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
      msa183564.2{147_A909}  TATGGgTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
      msa183564.2{147_H36B}  TATGGgTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
    msa183564.2{147_1169NT}  TATGGtTCAG AAGCAAAGAA TATTTcGCAT GGTACACACG TTGCTGGTAT
                  Consensus  *****-**** ********** *****-**** ********** **********

                             801                                                850
      msa183564.2{147_COH1}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATaGTCTT CTTTTAGAAG
      msa183564.2{147_M732}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATaGTCTT CTTTTAGAAG
      msa183564.2{147_M781}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATaGTCTT CTTTTAGAAG
      msa183564.2{147_2603}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
 msa183564.2{147_JM9130013}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
    msa183564.2{147_18RS21}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
       msa183564.2{147_090}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
    msa183564.2{147_CJB110}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
      msa183564.2{147_A909}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
      msa183564.2{147_H36B}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
    msa183564.2{147_1169NT}  TTTTGTAGGT AATAGTAAAC GTCCAGCAAT CAATgGTCTT CTTTTAGAAG
                  Consensus  ********** ********** ********** ****-***** **********

                             851                                                900
      msa183564.2{147_COH1}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
      msa183564.2{147_M732}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
      msa183564.2{147_M781}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
      msa183564.2{147_2603}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
 msa183564.2{147_JM9130013}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
    msa183564.2{147_18RS21}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
       msa183564.2{147_090}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
    msa183564.2{147_CJB110}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
      msa183564.2{147_A909}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
      msa183564.2{147_H36B}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
    msa183564.2{147_1169NT}  GTGCAGCGCC AAATGCTCAA GTCTTATTAA TGCGTATTCC AGATAAAATT
                  Consensus  ********** ********** ********** ********** **********

                             901                                                950
      msa183564.2{147_COH1}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA tAGACGCTGT
      msa183564.2{147_M732}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA tAGACGCTGT
      msa183564.2{147_M781}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA tAGACGCTGT
      msa183564.2{147_2603}  GATTCGGACA AATTTGGtGA AGCATATGCT AAAGCAATCA cAGACGCTGT
 msa183564.2{147_JM9130013}  GATTCGGACA AATTTGGtGA AGCATATGCT AAAGCAATCA cAGACGCTGT
    msa183564.2{147_18RS21}  GATTCGGACA AATTTGGtGA AGCATATGCT AAAGCAATCA cAGACGCTGT
       msa183564.2{147_090}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA cAGACGCTGT
    msa183564.2{147_CJB110}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA cAGACGCTGT
      msa183564.2{147_A909}  GATTCGGACA AATTTGGtGA AGCATATGCT AAAGCAATCA cAGACGCTGT
      msa183564.2{147_H36B}  GATTCGGACA AATTTGGtGA AGCATATGCT AAAGCAATCA cAGACGCTGT
    msa183564.2{147_1169NT}  GATTCGGACA AATTTGGaGA AGCATATGCT AAAGCAATCA cAGACGCTGT
                  Consensus  ********** *******-** ********** ********** -*********

                             951                                               1000
      msa183564.2{147_COH1}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTgGGAAAA ACgGCtGATT
      msa183564.2{147_M732}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTgGGAAAA ACgGCtGATT
      msa183564.2{147_M781}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTgGGAAAA ACgGCtGATT
      msa183564.2{147_2603}  TAATCTAGGA GCaAAAACGA TTAATATGAG taTtGGAAAA ACaGCtGATT
 msa183564.2{147_JM9130013}  TAATCTAGGA GCaAAAACGA TTAATATGAG taTtGGAAAA ACaGCtGATT
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
   msa183564.2{147_18RS21}  TAATCTAGGA GCaAAAACGA TTAATATGAG taTtGGAAAA ACaGCtGATT
      msa183564.2{147_090}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTtGGAAAA ACaGCaGATT
   msa183564.2{147_CJB110}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTtGGAAAA ACaGCaGATT
     msa183564.2{147_A909}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTtGGAAAA ACaGCaGATT
     msa183564.2{147_H36B}  TAATCTAGGA GCaAAAACGA TTAATATGAG ccTtGGAAAA ACaGCaGATT
   msa183564.2{147_1169NT}  TAATCTAGGA GCtAAAACGA TTAATATGAG taTtGGAAAA ACaGCtGATT
                 Consensus  ********** **_******* ********** __*_****** **_**_****

                            1001                                              1050
     msa183564.2{147_COH1}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
     msa183564.2{147_M732}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
     msa183564.2{147_M781}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
     msa183564.2{147_2603}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
 msa183564.2{147_JM9130013}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
   msa183564.2{147_18RS21}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
      msa183564.2{147_090}  CTTTAATTGC aCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
   msa183564.2{147_CJB110}  CTTTAATTGC aCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
     msa183564.2{147_A909}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
     msa183564.2{147_H36B}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
   msa183564.2{147_1169NT}  CTTTAATTGC tCTCAATGAT AAAGTTAAAT TAGCACTTAA ATTAGCTTCT
                 Consensus  ********** _********* ********** ********** **********

                            1051                                              1100
     msa183564.2{147_COH1}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
     msa183564.2{147_M732}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
     msa183564.2{147_M781}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
     msa183564.2{147_2603}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GcGCATTTGG
 msa183564.2{147_JM9130013}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GcGCATTTGG
   msa183564.2{147_18RS21}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GcGCATTTGG
      msa183564.2{147_090}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
   msa183564.2{147_CJB110}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
     msa183564.2{147_A909}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
     msa183564.2{147_H36B}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GtGCATTTGG
   msa183564.2{147_1169NT}  GAGAAGGGCG TTGCAGTTGT TGTGGCTGCC GGAAATGAAG GcGCATTTGG
                 Consensus  ********** ********** ********** ********** *_********

                            1101                                              1150
     msa183564.2{147_COH1}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
     msa183564.2{147_M732}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
     msa183564.2{147_M781}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
     msa183564.2{147_2603}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
 msa183564.2{147_JM9130013}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
   msa183564.2{147_18RS21}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
      msa183564.2{147_090}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
   msa183564.2{147_CJB110}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
     msa183564.2{147_A909}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
     msa183564.2{147_H36B}  TATGGATTAT AGCAAACCaT TATCAACTAA TCCTGACTAC GGTACGGTTA
   msa183564.2{147_1169NT}  TATGGATTAT AGCAAACCgT TATCAACTAA TCCTGACTAC GGTACGGTTA
                 Consensus  ********** ********_* ********** ********** **********

                            1151                                              1200
     msa183564.2{147_COH1}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
     msa183564.2{147_M732}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
     msa183564.2{147_M781}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
     msa183564.2{147_2603}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
 msa183564.2{147_JM9130013}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
   msa183564.2{147_18RS21}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
      msa183564.2{147_090}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
   msa183564.2{147_CJB110}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
     msa183564.2{147_A909}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
     msa183564.2{147_H36B}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
   msa183564.2{147_1169NT}  ATAGTCCAGC TATTTCTGAA GATACTTTGA GTGTTGCTAG CTATGAATCA
                 Consensus  ********** ********** ********** ********** **********

                            1201                                              1250
     msa183564.2{147_COH1}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
     msa183564.2{147_M732}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
     msa183564.2{147_M781}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
     msa183564.2{147_2603}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
 msa183564.2{147_JM9130013}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
   msa183564.2{147_18RS21}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
      msa183564.2{147_090}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
   msa183564.2{147_CJB110}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
     msa183564.2{147_A909}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
     msa183564.2{147_H36B}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
   msa183564.2{147_1169NT}  CTTAAAACTA TCAGTGAGGT CGTTGAAACA ACTATTGAAG GTAAGTTAGT
                 Consensus  ********** ********** ********** ********** **********

                            1251                                              1300
     msa183564.2{147_COH1}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
     msa183564.2{147_M732}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
     msa183564.2{147_M781}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
     msa183564.2{147_2603}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
msa183564.2{147_JM9130013}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
   msa183564.2{147_18RS21}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
      msa183564.2{147_090}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
   msa183564.2{147_CJB110}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
     msa183564.2{147_A909}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
     msa183564.2{147_H36B}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
   msa183564.2{147_1169NT}  TAAGTTGCCG ATTGTGACTT CTAAACCTTT TGACAAAGGT AAGGCCTACG
                 Consensus  ********** ********** ********** ********** **********

                            1301                                              1350
     msa183564.2{147_COH1}  ATGTGGTTTA TGCCAATTAT GGTGC..AAA AAAGAtTTTG AAGGTAAGGA
     msa183564.2{147_M732}  ATGTGGTTTA TGCCAATTAT GGTGC..AAA AAAGAtTTTG AAGGTAAGGA
     msa183564.2{147_M781}  ATGTGGTTTA TGCCAATTAT GGTGC..AAA AAAGAtTTTG AAGGTAAGGA
     msa183564.2{147_2603}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
msa183564.2{147_JM9130013}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
   msa183564.2{147_18RS21}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
      msa183564.2{147_090}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
   msa183564.2{147_CJB110}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
     msa183564.2{147_A909}  ATGTGGTTTA TGCCAATTAT GGTGCaaAAA AAAGAcTTTG AAGGTAAGGA
     msa183564.2{147_H36B}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
   msa183564.2{147_1169NT}  ATGTGGTTTA TGCCAATTAT GGTGC.aAAA AAAGAcTTTG AAGGTAAGGA
                 Consensus  ********** ********** *****--*** *****-**** **********

                            1351                                              1400
     msa183564.2{147_COH1}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
     msa183564.2{147_M732}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
     msa183564.2{147_M781}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
     msa183564.2{147_2603}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
msa183564.2{147_JM9130013}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
   msa183564.2{147_18RS21}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
      msa183564.2{147_090}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
   msa183564.2{147_CJB110}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
     msa183564.2{147_A909}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
     msa183564.2{147_H36B}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
   msa183564.2{147_1169NT}  CTTTAAAGGT AAGATTGCAT TAATTGAGCG TGGTGGTGGA CTTGATTTTA
                 Consensus  ********** ********** ********** ********** **********

                            1401                                              1450
     msa183564.2{147_COH1}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
     msa183564.2{147_M732}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
     msa183564.2{147_M781}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
     msa183564.2{147_2603}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
msa183564.2{147_JM9130013}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
   msa183564.2{147_18RS21}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
      msa183564.2{147_090}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
   msa183564.2{147_CJB110}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
     msa183564.2{147_A909}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
     msa183564.2{147_H36B}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
   msa183564.2{147_1169NT}  TGACTAAAAT CACTCATGCT ACAAATGCAG GTGTTGTTGG TATCGTTATT
                 Consensus  ********** ********** ********** ********** **********

                            1451                                              1500
     msa183564.2{147_COH1}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
     msa183564.2{147_M732}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
     msa183564.2{147_M781}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
     msa183564.2{147_2603}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
msa183564.2{147_JM9130013}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
   msa183564.2{147_18RS21}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
      msa183564.2{147_090}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
   msa183564.2{147_CJB110}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
     msa183564.2{147_A909}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
     msa183564.2{147_H36B}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
   msa183564.2{147_1169NT}  TTTAACGATC AAGAAAAACG TGGAAATTTT CTAATTCCTT ACCGTGAATT
                 Consensus  ********** ********** ********** ********** **********

                            1501                                              1550
     msa183564.2{147_COH1}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
     msa183564.2{147_M732}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
     msa183564.2{147_M781}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
     msa183564.2{147_2603}  ACCTGTGGGG aTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
msa183564.2{147_JM9130013}  ACCTGTGGGG aTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
   msa183564.2{147_18RS21}  ACCTGTGGGG aTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
      msa183564.2{147_090}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
   msa183564.2{147_CJB110}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
     msa183564.2{147_A909}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
     msa183564.2{147_H36B}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
   msa183564.2{147_1169NT}  ACCTGTGGGG gTTATTAGTA AAGTAGATGG CGAGCGTATA AAAAATACTT
                 Consensus  ********** -********* ********** ********** **********

                            1551                                              1600
     msa183564.2{147_COH1}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
     msa183564.2{147_M732}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
     msa183564.2{147_M781}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
    msa183564.2{147_2603}   CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_JM9130013}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
   msa183564.2{147_18RS21}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
     msa183564.2{147_090}   CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
   msa183564.2{147_CJB110}  CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
    msa183564.2{147_A909}   CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
    msa183564.2{147_H36B}   CAAGTCAGTT AACATTTAAC CAGAGtTTTG AAGTAGTTGA TAGCCAAGGT
   msa183564.2{147_1169NT}  CAAGTCAGTT AACATTTAAC CAGAGaTTTG AAGTAGTTGA TAGCCAAGGT
                Consensus   ********** ********** *****-**** ********** **********

                            1601                                              1650
    msa183564.2{147_COH1}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
    msa183564.2{147_M732}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
    msa183564.2{147_M781}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
    msa183564.2{147_2603}   GGtAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
msa183564.2{147_JM9130013}  GGtAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
   msa183564.2{147_18RS21}  GGtAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
     msa183564.2{147_090}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
   msa183564.2{147_CJB110}  GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
    msa183564.2{147_A909}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
    msa183564.2{147_H36B}   GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
   msa183564.2{147_1169NT}  GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCGTGACAG CTGAAGGAGC
                Consensus   **-******* ********** ********** ********** **********

                            1651                                              1700
    msa183564.2{147_COH1}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
    msa183564.2{147_M732}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
    msa183564.2{147_M781}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
    msa183564.2{147_2603}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_JM9130013}  AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
   msa183564.2{147_18RS21}  AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
     msa183564.2{147_090}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
   msa183564.2{147_CJB110}  AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
    msa183564.2{147_A909}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
    msa183564.2{147_H36B}   AATCAAGCCT GATGTAACAG CTTCTGGCTT tGAAATTTAT TCTTCAACCT
   msa183564.2{147_1169NT}  AATCAAGCCT GATGTAACAG CTTCTGGCTT cGAAATTTAT TCTTCAACCT
                Consensus   ********** ********** ********** -********* **********

                            1701                                              1750
    msa183564.2{147_COH1}   ATAATAATCA ATACtAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
    msa183564.2{147_M732}   ATAATAATCA ATACtAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
    msa183564.2{147_M781}   ATAATAATCA ATACtAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
    msa183564.2{147_2603}   ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
msa183564.2{147_JM9130013}  ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
   msa183564.2{147_18RS21}  ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
     msa183564.2{147_090}   ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
   msa183564.2{147_CJB110}  ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
    msa183564.2{147_A909}   ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
    msa183564.2{147_H36B}   ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
   msa183564.2{147_1169NT}  ATAATAATCA ATACcAAACA ATGTCTGGTA CAAGTATGGC TTCACCACAT
                Consensus   ********** ****-***** ********** ********** **********

                            1751                                              1800
    msa183564.2{147_COH1}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
    msa183564.2{147_M732}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
    msa183564.2{147_M781}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
    msa183564.2{147_2603}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
msa183564.2{147_JM9130013}  GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
   msa183564.2{147_18RS21}  GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
     msa183564.2{147_090}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
   msa183564.2{147_CJB110}  GTTGCAGGAT TAATGACAAT GCTTCAAAaT CATTTGGCTG AGAAATATAA
    msa183564.2{147_A909}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
    msa183564.2{147_H36B}   GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
   msa183564.2{147_1169NT}  GTTGCAGGAT TAATGACAAT GCTTCAAAgT CATTTGGCTG AGAAATATAA
                Consensus   ********** ********** ********-* ********** **********

                            1801                                              1850
    msa183564.2{147_COH1}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
    msa183564.2{147_M732}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
    msa183564.2{147_M781}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
    msa183564.2{147_2603}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
msa183564.2{147_JM9130013}  AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
   msa183564.2{147_18RS21}  AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
     msa183564.2{147_090}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
   msa183564.2{147_CJB110}  AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
    msa183564.2{147_A909}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
    msa183564.2{147_H36B}   AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
   msa183564.2{147_1169NT}  AGGGATGAAT TTAGATTCTA AAAAATTGCT AGAATTGTCT AAAAACATCC
                Consensus   ********** ********** ********** ********** **********

                            1851                                              1900
    msa183564.2{147_COH1}   TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
    msa183564.2{147_M732}   TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
      msa183564.2{147_M781}   TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
      msa183564.2{147_2603}   TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
  msa183564.2{147_JM9130013}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
     msa183564.2{147_18RS21}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
        msa183564.2{147_090}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
     msa183564.2{147_CJB110}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
       msa183564.2{147_A909}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
       msa183564.2{147_H36B}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
     msa183564.2{147_1169NT}  TCATGAGCTC AGCAACAGCA TTATATAGTG AAGAGGATAA GGCGTTTTAT
                   Consensus  ********** ********** ********** ********** **********

                              1901                                              1950
       msa183564.2{147_COH1}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
       msa183564.2{147_M732}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
       msa183564.2{147_M781}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
       msa183564.2{147_2603}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
  msa183564.2{147_JM9130013}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
     msa183564.2{147_18RS21}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
        msa183564.2{147_090}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
     msa183564.2{147_CJB110}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
       msa183564.2{147_A909}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
       msa183564.2{147_H36B}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
     msa183564.2{147_1169NT}  TCACCACGTC AGCAAGGTGC AGGTGTAGTT GATGCTGAAA AAGCTATCCA
                   Consensus  ********** ********** ********** ********** **********

                              1951                                              2000
       msa183564.2{147_COH1}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGtTAAA ATTAATCTCA
       msa183564.2{147_M732}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGtTAAA ATTAATCTCA
       msa183564.2{147_M781}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGtTAAA ATTAATCTCA
       msa183564.2{147_2603}  AGCTCAATAT TATaTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
  msa183564.2{147_JM9130013}  AGCTCAATAT TATaTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
     msa183564.2{147_18RS21}  AGCTCAATAT TATaTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
        msa183564.2{147_090}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
     msa183564.2{147_CJB110}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
       msa183564.2{147_A909}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
       msa183564.2{147_H36B}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
     msa183564.2{147_1169NT}  AGCTCAATAT TATgTTACTG GAAACGATGG CAAAGcTAAA ATTAATCTCA
                   Consensus  ********** ***_****** ********** *****_**** **********

                              2001                                              2050
       msa183564.2{147_COH1}  AACGAgaGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
       msa183564.2{147_M732}  AACGAgaGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
       msa183564.2{147_M781}  AACGAgaGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
       msa183564.2{147_2603}  AACGAatGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
  msa183564.2{147_JM9130013}  AACGAatGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
     msa183564.2{147_18RS21}  AACGAatGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
        msa183564.2{147_090}  AACGAgtGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
     msa183564.2{147_CJB110}  AACGAgtGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
       msa183564.2{147_A909}  AACGAgtGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
       msa183564.2{147_H36B}  AACGAgtGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
     msa183564.2{147_1169NT}  AACGAgtGGG AGATAAATTT GATATCACAG TTACAATTCA TAAACTTGTA
                   Consensus  *****__*** ********** ********** ********** **********

                              2051                                              2100
       msa183564.2{147_COH1}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
       msa183564.2{147_M732}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
       msa183564.2{147_M781}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
       msa183564.2{147_2603}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
  msa183564.2{147_JM9130013}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
     msa183564.2{147_18RS21}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
        msa183564.2{147_090}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
     msa183564.2{147_CJB110}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
       msa183564.2{147_A909}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
       msa183564.2{147_H36B}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
     msa183564.2{147_1169NT}  GAAGGTGTCA AAGAATTGTA TTATCAAGCT AATGTAGCAA CAGAACAAGT
                   Consensus  ********** ********** ********** ********** **********

                              2101                                              2150
       msa183564.2{147_COH1}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
       msa183564.2{147_M732}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
       msa183564.2{147_M781}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
       msa183564.2{147_2603}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
  msa183564.2{147_JM9130013}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
     msa183564.2{147_18RS21}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
        msa183564.2{147_090}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
     msa183564.2{147_CJB110}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
       msa183564.2{147_A909}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
       msa183564.2{147_H36B}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
     msa183564.2{147_1169NT}  AAATAAAGGT AAATTTGCCC TTAAACCACA AGCCTTGCTA GATACTAATT
                   Consensus  ********** ********** ********** ********** **********

                              2151                                              2200
       msa183564.2{147_COH1}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
      msa183564.2{147_M732}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
      msa183564.2{147_M781}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
      msa183564.2{147_2603}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
  msa183564.2{147_JM9130013} GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
     msa183564.2{147_18RS21} GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
       msa183564.2{147_090}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
     msa183564.2{147_CJB110} GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
      msa183564.2{147_A909}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
      msa183564.2{147_H36B}  GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
     msa183564.2{147_1169NT} GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT
                   Consensus ********** ********** ********** ********** **********

                             2201                                              2250
      msa183564.2{147_COH1}  GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
      msa183564.2{147_M732}  GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
      msa183564.2{147_M781}  GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
      msa183564.2{147_2603}  GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
  msa183564.2{147_JM9130013} GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
     msa183564.2{147_18RS21} GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
       msa183564.2{147_090}  GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
     msa183564.2{147_CJB110} GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
      msa183564.2{147_A909}  GATtCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
      msa183564.2{147_H36B}  GATtCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
     msa183564.2{147_1169NT} GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA
                   Consensus ***-****** ********** ********** ********** **********

                             2251                                              2300
      msa183564.2{147_COH1}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
      msa183564.2{147_M732}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
      msa183564.2{147_M781}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
      msa183564.2{147_2603}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
  msa183564.2{147_JM9130013} TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
     msa183564.2{147_18RS21} TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
       msa183564.2{147_090}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
     msa183564.2{147_CJB110} TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
      msa183564.2{147_A909}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
      msa183564.2{147_H36B}  TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG
     msa183564.2{147_1169NT} TTTCTTAGAA GGTTTTGTAC GTTTTAAAGA AGCtAAGGAT AGTAATCAGG
                   Consensus ********** ********** ********** ***-****** **********

                             2301                                              2350
      msa183564.2{147_COH1}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
      msa183564.2{147_M732}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
      msa183564.2{147_M781}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
      msa183564.2{147_2603}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
  msa183564.2{147_JM9130013} AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
     msa183564.2{147_18RS21} AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
       msa183564.2{147_090}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
     msa183564.2{147_CJB110} AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
      msa183564.2{147_A909}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
      msa183564.2{147_H36B}  AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA
     msa183564.2{147_1169NT} AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAgCTTA
                   Consensus ********** ********** ********** ********** *****-****

                             2351                                              2400
      msa183564.2{147_COH1}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
      msa183564.2{147_M732}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
      msa183564.2{147_M781}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
      msa183564.2{147_2603}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
  msa183564.2{147_JM9130013} CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
     msa183564.2{147_18RS21} CAAGCACTTG AAACACCGAT TTATAAGACG aTTTCTAAAG GTAGTTTCTA
       msa183564.2{147_090}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
     msa183564.2{147_CJB110} CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
      msa183564.2{147_A909}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
      msa183564.2{147_H36B}  CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
     msa183564.2{147_1169NT} CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA
                   Consensus ********** ********** ********** -********* **********

                             2401                                              2450
      msa183564.2{147_COH1}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
      msa183564.2{147_M732}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
      msa183564.2{147_M781}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
      msa183564.2{147_2603}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
  msa183564.2{147_JM9130013} CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
     msa183564.2{147_18RS21} CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
       msa183564.2{147_090}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
     msa183564.2{147_CJB110} CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
      msa183564.2{147_A909}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
      msa183564.2{147_H36B}  CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT
     msa183564.2{147_1169NT} CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAtAATGAAT
                   Consensus ********** ********** ********** ********** **-*******

                             2451                                              2500
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
     msa183564.2{147_COH1}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
     msa183564.2{147_M732}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
     msa183564.2{147_M781}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
     msa183564.2{147_2603}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
msa183564.2{147_JM9130013}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
   msa183564.2{147_18RS21}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
      msa183564.2{147_090}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
   msa183564.2{147_CJB110}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
     msa183564.2{147_A909}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
     msa183564.2{147_H36B}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
   msa183564.2{147_1169NT}  CAGCTCCTTT TGAAAGCAAC AACTATACTG CCTTGTTAAC ACAATCAGCG
                 Consensus  ********** ********** ********** ********** **********

                            2501                                              2550
     msa183564.2{147_COH1}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
     msa183564.2{147_M732}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
     msa183564.2{147_M781}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
     msa183564.2{147_2603}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
msa183564.2{147_JM9130013}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
   msa183564.2{147_18RS21}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
      msa183564.2{147_090}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
   msa183564.2{147_CJB110}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
     msa183564.2{147_A909}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
     msa183564.2{147_H36B}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
   msa183564.2{147_1169NT}  TCTTGGGGCT ATGTTGATTA TGTCAAAAAT GGTGGGGAGT TAGAATTAGC
                 Consensus  ********** ********** ********** ********** **********

                            2551                                              2600
     msa183564.2{147_COH1}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
     msa183564.2{147_M732}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
     msa183564.2{147_M781}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
     msa183564.2{147_2603}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
msa183564.2{147_JM9130013}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
   msa183564.2{147_18RS21}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
      msa183564.2{147_090}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
   msa183564.2{147_CJB110}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
     msa183564.2{147_A909}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
     msa183564.2{147_H36B}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
   msa183564.2{147_1169NT}  ACCGGAGAGT CCAAAAAGAA TTATTTTAGG AACTTTTGAG AATAAGGTTG
                 Consensus  ********** ********** ********** ********** **********

                            2601                                              2650
     msa183564.2{147_COH1}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
     msa183564.2{147_M732}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
     msa183564.2{147_M781}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
     msa183564.2{147_2603}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
msa183564.2{147_JM9130013}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
   msa183564.2{147_18RS21}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
      msa183564.2{147_090}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
   msa183564.2{147_CJB110}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
     msa183564.2{147_A909}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
     msa183564.2{147_H36B}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
   msa183564.2{147_1169NT}  AGGATAAAAC AATTCATCTT TTGGAAAGAG ATGCAGCGAA TAATCCATAT
                 Consensus  ********** ********** ********** ********** **********

                            2651                                              2700
     msa183564.2{147_COH1}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
     msa183564.2{147_M732}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
     msa183564.2{147_M781}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
     msa183564.2{147_2603}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
msa183564.2{147_JM9130013}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
   msa183564.2{147_18RS21}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAcGAAA TCACTCCCCA
      msa183564.2{147_090}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAtGAAA TCACTCCCCA
   msa183564.2{147_CJB110}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAtGAAA TCACTCCCCA
     msa183564.2{147_A909}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAtGAAA TCACTCCCCA
     msa183564.2{147_H36B}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAtGAAA TCACTCCCCA
   msa183564.2{147_1169NT}  TTTGCCATTT CTCCAAATAA AGATGGAAAT AGGGAtGAAA TCACTCCCCA
                 Consensus  ********** ********** ********** *****-**** **********

                            2701                                              2750
     msa183564.2{147_COH1}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
     msa183564.2{147_M732}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
     msa183564.2{147_M781}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
     msa183564.2{147_2603}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
msa183564.2{147_JM9130013}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
   msa183564.2{147_18RS21}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
      msa183564.2{147_090}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
   msa183564.2{147_CJB110}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
     msa183564.2{147_A909}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
     msa183564.2{147_H36B}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
   msa183564.2{147_1169NT}  GGCAACTTTC TTAAGAAATG TTAAGGATAT TTCTGCTCAA GTTCTAGATC
                 Consensus  ********** ********** ********** ********** **********
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
                            2751                                               2800
    msa183564.2{147_COH1}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
    msa183564.2{147_M732}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
    msa183564.2{147_M781}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
    msa183564.2{147_2603}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
msa183564.2{147_JM9130013}  AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
  msa183564.2{147_18RS21}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
     msa183564.2{147_090}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
  msa183564.2{147_CJB110}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
    msa183564.2{147_A909}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
    msa183564.2{147_H36B}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
  msa183564.2{147_1169NT}   AAAATGGAAA TGTTATTTGG CAAAGTAAGG TTTTACCATC TTATCGTAAA
                Consensus   ********** ********** ********** ********** **********

                            2801                                               2850
    msa183564.2{147_COH1}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
    msa183564.2{147_M732}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
    msa183564.2{147_M781}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
    msa183564.2{147_2603}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
msa183564.2{147_JM9130013}  AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
  msa183564.2{147_18RS21}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
     msa183564.2{147_090}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
  msa183564.2{147_CJB110}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
    msa183564.2{147_A909}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
    msa183564.2{147_H36B}   AATTTCCATA ATAATCCAAA GCAaAGTGAT GGTCATTATC GTATGGATGC
  msa183564.2{147_1169NT}   AATTTCCATA ATAATCCAAA GCAgAGTGAT GGTCATTATC GTATGGATGC
                Consensus   ********** ********** ***-****** ********** **********

                            2851                                               2900
    msa183564.2{147_COH1}   tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
    msa183564.2{147_M732}   tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
    msa183564.2{147_M781}   tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
    msa183564.2{147_2603}   tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
msa183564.2{147_JM9130013}  tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
  msa183564.2{147_18RS21}   tcTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
     msa183564.2{147_090}   ctTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
  msa183564.2{147_CJB110}   ctTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
    msa183564.2{147_A909}   ccTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
    msa183564.2{147_H36B}   ccTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
  msa183564.2{147_1169NT}   ccTTCAGTGG AGTGGTTTAG ATAAGGATGG CAAAGTTGTA GCAGATGGTT
                Consensus   --******** ********** ********** ********** **********

                            2901                                               2950
    msa183564.2{147_COH1}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
    msa183564.2{147_M732}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
    msa183564.2{147_M781}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
    msa183564.2{147_2603}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
msa183564.2{147_JM9130013}  TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
  msa183564.2{147_18RS21}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
     msa183564.2{147_090}   TTTATACTTA TCGccTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
  msa183564.2{147_CJB110}   TTTATACTTA TCGccTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
    msa183564.2{147_A909}   TTTATACTTA TCGttTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
    msa183564.2{147_H36B}   TTTATACTTA TCGttTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
  msa183564.2{147_1169NT}   TTTATACTTA TCGctTACGT TACACACCAG TAGCAGAAGG AGCAAATAGT
                Consensus   ********** ***--***** ********** ********** **********

                            2951                                               3000
    msa183564.2{147_COH1}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
    msa183564.2{147_M732}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
    msa183564.2{147_M781}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
    msa183564.2{147_2603}   CAGGAGTCAG ACTTTAAAGT aCAAGTAAGT ACTAAGTCAC CAAATCTTCC
msa183564.2{147_JM9130013}  CAGGAGTCAG ACTTTAAAGT aCAAGTAAGT ACTAAGTCAC CAAATCTTCC
  msa183564.2{147_18RS21}   CAGGAGTCAG ACTTTAAAGT aCAAGTAAGT ACTAAGTCAC CAAATCTTCC
     msa183564.2{147_090}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
  msa183564.2{147_CJB110}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
    msa183564.2{147_A909}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
    msa183564.2{147_H36B}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
  msa183564.2{147_1169NT}   CAGGAGTCAG ACTTTAAAGT tCAAGTAAGT ACTAAGTCAC CAAATCTTCC
                Consensus   ********** ********** -********* ********** **********

                            3001                                               3050
    msa183564.2{147_COH1}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
    msa183564.2{147_M732}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
    msa183564.2{147_M781}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
    msa183564.2{147_2603}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
msa183564.2{147_JM9130013}  TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
  msa183564.2{147_18RS21}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
     msa183564.2{147_090}   TTtACtAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
  msa183564.2{147_CJB110}   TTtACtAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
    msa183564.2{147_A909}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
    msa183564.2{147_H36B}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
  msa183564.2{147_1169NT}   TTcACgAGCT CAGTTTGATG AAACTAATCG AACATTAAGC TTAGCCATGC
                Consensus   **-**-**** ********** ********** ********** **********
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
                            3051                                              3100
     msa183564.2{147_COH1}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
     msa183564.2{147_M732}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
     msa183564.2{147_M781}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
     msa183564.2{147_2603}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
msa183564.2{147_JM9130013}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
   msa183564.2{147_18RS21}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
      msa183564.2{147_090}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
   msa183564.2{147_CJB110}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTTTTATCT
     msa183564.2{147_A909}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTTTTATCT
     msa183564.2{147_H36B}  CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTTTTATCT
   msa183564.2{147_1169NT}  CTAAGGgAAG TAGTTATGTT CCTAtATATC GTcTACAATT AGTTTTATCT
                 Consensus  ******_*** ********** ****_***** **_******* **********

                            3101                                              3150
     msa183564.2{147_COH1}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
     msa183564.2{147_M732}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
     msa183564.2{147_M781}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
     msa183564.2{147_2603}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
msa183564.2{147_JM9130013}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
   msa183564.2{147_18RS21}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
      msa183564.2{147_090}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
   msa183564.2{147_CJB110}  CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT ACcATTATTT
     msa183564.2{147_A909}  CATGTTGTAA AAGATGAAGA ATATGGaGAT GAGACTTCTT ACcATTATTT
     msa183564.2{147_H36B}  CATGTTGTAA AAGATGAAGA ATATGGaGAT GAGACTTCTT ACcATTATTT
   msa183564.2{147_1169NT}  CATGTTGTAA AAGATGAAGA ATATGGaGAT GAGACTTCTT ACtATTATTT
                 Consensus  ********** ********** ******_*** ********** **_*******

                            3151                                              3200
     msa183564.2{147_COH1}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
     msa183564.2{147_M732}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
     msa183564.2{147_M781}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
     msa183564.2{147_2603}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
msa183564.2{147_JM9130013}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
   msa183564.2{147_18RS21}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
      msa183564.2{147_090}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
   msa183564.2{147_CJB110}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG
     msa183564.2{147_A909}  CCATATAGAT CgAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAGATAG
     msa183564.2{147_H36B}  CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAGATAG
   msa183564.2{147_1169NT}  CCATATAGAT CaAGAAGGTA AAGcGACACT TCCTAAAACg GTTAAGATAG
                 Consensus  ********** *_******** ***_****** *********_ **********

                            3201                                              3250
     msa183564.2{147_COH1}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
     msa183564.2{147_M732}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
     msa183564.2{147_M781}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
     msa183564.2{147_2603}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
msa183564.2{147_JM9130013}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
   msa183564.2{147_18RS21}  GAGAGAGTGA GGTTGCgGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
      msa183564.2{147_090}  GAGAGAGTGA GGTTGCaGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
   msa183564.2{147_CJB110}  GAGAGAGTGA GGTTGCaGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
     msa183564.2{147_A909}  GAGAGAGTGA GGTTGCaGTA GACCCTAAGa CCTTGACACT TGTTGTGGAA
     msa183564.2{147_H36B}  GAGAGAGTGA GGTTGCaGTA GACCCTAAGa CCTTGACACT TGTTGTGGAA
   msa183564.2{147_1169NT}  GAGAGAGTGA GGTTGCaGTA GACCCTAAGg CCTTGACACT TGTTGTGGAA
                 Consensus  ********** ******_*** *********_ ********** **********

                            3251                                              3300
     msa183564.2{147_COH1}  GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
     msa183564.2{147_M732}  GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
     msa183564.2{147_M781}  GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
     msa183564.2{147_2603}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAtC TCTTGAATAA
msa183564.2{147_JM9130013}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAtC TCTTGAATAA
   msa183564.2{147_18RS21}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAtC TCTTGAATAA
      msa183564.2{147_090}  GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
   msa183564.2{147_CJB110}  GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
     msa183564.2{147_A909}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
     msa183564.2{147_H36B}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
   msa183564.2{147_1169NT}  GATAAAGCTG GTAATTTcGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA
                 Consensus  ********** *******_** ********** ********_* **********

                            3301                                              3350
     msa183564.2{147_COH1}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
     msa183564.2{147_M732}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
     msa183564.2{147_M781}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
     msa183564.2{147_2603}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
msa183564.2{147_JM9130013}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
   msa183564.2{147_18RS21}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
      msa183564.2{147_090}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
   msa183564.2{147_CJB110}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
     msa183564.2{147_A909}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAaTTTCA
     msa183564.2{147_H36B}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAaTTTCA
   msa183564.2{147_1169NT}  GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

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                 Consensus  ********** ********** ********** ********** ****_*****

                            3351                                              3400
     msa183564.2{147_COH1}  AATATTTTGA TAACTTGAAg AAAGAAcCTA TGTTTATTTC TAAAgAAGgA
     msa183564.2{147_M732}  AATATTTTGA TAACTTGAAg AAAGAAcCTA TGTTTATTTC TAAAgAAGgA
     msa183564.2{147_M781}  AATATTTTGA TAACTTGAAg AAAGAAcCTA TGTTTATTTC TAAAgAAGgA
     msa183564.2{147_2603}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAaAAGaA
msa183564.2{147_JM9130013}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAaAAGaA
   msa183564.2{147_18RS21}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAaAAGaA
    msa183564.2{147_090}    AATATTTTGA TAACTTGAAa AAAGAAtCTA TGTTTATTTC TAAAgAAGgA
   msa183564.2{147_CJB110}  AATATTTTGA TAACTTGAAa AAAGAAtCTA TGTTTATTTC TAAAgAAGgA
     msa183564.2{147_A909}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAgAAGgA
     msa183564.2{147_H36B}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAgAAGgA
   msa183564.2{147_1169NT}  AATATTTTGA TAACTTGAAa AAAGAAcCTA TGTTTATTTC TAAAaAAGaA
                 Consensus  ********** *********_ ******_*** ********** ****_***_*

                            3401                                              3450
     msa183564.2{147_COH1}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA acATTAGTTA AGCCtCAaAC
     msa183564.2{147_M732}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA acATTAGTTA AGCCtCAaAC
     msa183564.2{147_M781}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA acATTAGTTA AGCCtCAaAC
     msa183564.2{147_2603}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA atATTAGTTA AGCCgCAaAC
msa183564.2{147_JM9130013}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA atATTAGTTA AGCCgCAaAC
   msa183564.2{147_18RS21}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA atATTAGTTA AGCCgCAaAC
    msa183564.2{147_090}    AAAGTAGTAA ACAAGAATCT AGAAGAAATA acATTAGTTA AGCCgCAaAC
   msa183564.2{147_CJB110}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA acATTAGTTA AGCCgCAaAC
     msa183564.2{147_A909}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA gcATTAGTTA AGCCgCAaAC
     msa183564.2{147_H36B}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA gcATTAGTTA AGCCgCAaAC
   msa183564.2{147_1169NT}  AAAGTAGTAA ACAAGAATCT AGAAGAAATA atATTAGTTA AGCCgCAcAC
                 Consensus  ********** ********** ********** __******** ****_**_**

                            3451                                              3500
     msa183564.2{147_COH1}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
     msa183564.2{147_M732}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
     msa183564.2{147_M781}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
     msa183564.2{147_2603}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
msa183564.2{147_JM9130013}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
   msa183564.2{147_18RS21}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
    msa183564.2{147_090}    TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
   msa183564.2{147_CJB110}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
     msa183564.2{147_A909}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTcAA TCAGGAAATG
     msa183564.2{147_H36B}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTcAA TCAGGAAATG
   msa183564.2{147_1169NT}  TACAGTTACT ACTCAATCAT TGTCTAAAGA AATAACTaAA TCAGGAAATG
                 Consensus  ********** ********** ********** *******_** **********

                            3501                                              3550
     msa183564.2{147_COH1}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
     msa183564.2{147_M732}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
     msa183564.2{147_M781}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
     msa183564.2{147_2603}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
msa183564.2{147_JM9130013}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
   msa183564.2{147_18RS21}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
    msa183564.2{147_090}    AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
   msa183564.2{147_CJB110}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
     msa183564.2{147_A909}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
     msa183564.2{147_H36B}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGcAGAGT AGCTAAgATC
   msa183564.2{147_1169NT}  AGAAAGTCCT CACTTCTACA AACAATAATA GTAGtAGAGT AGCTAAaATC
                 Consensus  ********** ********** ********** ****_***** ******_***

                            3551                                              3600
     msa183564.2{147_COH1}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
     msa183564.2{147_M732}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
     msa183564.2{147_M781}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
     msa183564.2{147_2603}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACCt tacctagtac
msa183564.2{147_JM9130013}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
   msa183564.2{147_18RS21}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
    msa183564.2{147_090}    ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
   msa183564.2{147_CJB110}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
     msa183564.2{147_A909}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
     msa183564.2{147_H36B}  ATATCACCTA AACATAAcGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
   msa183564.2{147_1169NT}  ATATCACCTA AACATAAtGG GGATTCTGTT AACCATACC~ ~~~~~~~~~~
                 Consensus  ********** *******_** ********** ********** **********

                            3601                                              3650
     msa183564.2{147_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_2603}  atcagataga gcaacgaatg gtctatttgt tggtactttg gcattgttat
msa183564.2{147_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa183564.2{147_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa183564.2{147_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa183564.2{147_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa183564.2{147_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
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Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
   msa183564.2{147_1169NT}  ---------- ---------- ---------- ---------- ----------
                 Consensus  ********** ********** ********** ********** **********

                            3651                                              3700
     msa183564.2{147_COH1}  ---------- ---------- ---------- ---------- ----------
     msa183564.2{147_M732}  ---------- ---------- ---------- ---------- ----------
     msa183564.2{147_M781}  ---------- ---------- ---------- ---------- ----------
     msa183564.2{147_2603}  ctagtttact tctttatttg aaacccaaaa agactaaaaa taatagtaaa
msa183564.2{147_JM9130013}  ---------- ---------- ---------- ---------- ----------
   msa183564.2{147_18RS21}  ---------- ---------- ---------- ---------- ----------
      msa183564.2{147_090}  ---------- ---------- ---------- ---------- ----------
   msa183564.2{147_CJB110}  ---------- ---------- ---------- ---------- ----------
     msa183564.2{147_A909}  ---------- ---------- ---------- ---------- ----------
     msa183564.2{147_H36B}  ---------- ---------- ---------- ---------- ----------
   msa183564.2{147_1169NT}  ---------- ---------- ---------- ---------- ----------
                 Consensus  ********** ********** ********** ********** **********
```

SEQ ID NO. 4412
STRAIN 2603
VDKHHSKKAILKLTLITTSILLMHSNQVNAEEQELKNQEQSPVIANVAQQPSPSVTTNTV
EKTSVTAASASNTAKEMGDTSVKNDKTEDELLEELSKNLDTSNLGADLEEEYPSKPETTN
NKESNVVTNASTAIAQKVPSAYEEVKPESKSSLAVLDTSKITKLQAITQRGKGNVVAIID
TGFDINHDIFRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWVNDKIVFAHNYANNTETV
ADIAAAMKDGYGSEAKNISHGTHVAGIFVGNSKRPAINGLLLEGAAPNAQVLLMRIPDKI
DSDKFGEAYAKAITDAVNLGAKTINMSIGKTADSLIALNDKVKLALKLASEKGVAVVVAA
GNEGAFGMDYSKPLSTNPDYGTVNSPAISEDTLSVASYESLKTISEVVETTIEGKLVKLP
IVTSKPFDKGKAYDVVYANYGAKKDFEGKDFKGKIALIERGGGLDFMTKITHATNAGVVG
IVIFNDQEKRGNFLIPYRELPVGIISKVDGERIKNTSSQLTFNQSFEVVDSQGGNRMLEQ
SSWGVTAEGAIKPDVTASGFEIYSSTYNNQYQTMSGTSMASPHVAGLMTMLQSHLAEKYK
GMNLDSKKLLELSKNILMSSATALYSEEDKAFYSPRQQGAGVVDAEKAIQAQYYITGNDG
KAKINLKRMGDKFDITVTIHKLVEGVKELYYQANVATEQVNKGKFALKPQALLDTNWQKV
ILRDKETQVRFTIDASQFSQKLKEQMANGYFLEGFVRFKEAKDSNQELMSIPFVGFNGDF
ANLQALETPIYKTLSKGSFYYKPNDTTHKDQLEYNESAPFESNNYTALLTQSASWGYVDY
VKNGGELELAPESPKRIILGTFENKVEDKTIHLLERDAANNPYFAISPNKDGNRDEITPQ
ATFLRNVKDISAQVLDQNGNVIWQSKVLPSYRKNFHNNPKQSDGHYRMDALQWSGLDKDG
KVVADGFYTYRLRYTPVAEGANSQESDFKVQVSTKSPNLPSRAQFDETNRTLSLAMPKES
SYVPTYRLQLVLSHVVKDEEYGDETSYHYFHIDQEGKVTLPKTVKIGESEVAVDPKALTL
VVEDKAGNFATVKLSDLLNKAVVSEKENAIVISNSFKYFDNLKKEPMFISKKEKVVNKNL
EEIILVKPQTTVTTQSLSKEITKSGNEKVLTSTNNNSSRVAKIISPKHNGDSVNHTLPST
SDRATNGLFVGTLALLSSLLLYLKPKKTKNNSK

SEQ ID NO. 4413
STRAIN A909
EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKRL.R.G
L.R.DCIN.AWWWT.FYD.NHSCYKCRCCWYRYF.RSRKTWKFSNSLP.ITCGGY..SRW
RAYKKYFKSVNI.PEF.SS..PRWQSYAGTIKLGRDS.RSNQA.CNSFWL.NLFFNL..S
IPNNVWYKYGFTTCCRINDNASKSFG.EI.RDEFRF.KIARIV.KHPHELSNSII..RG.
GVLFTTSARCRCS.C.KSYPSSILCYWKRWQS.N.SQTSGR.I.YHSYNS.TCRRCQRIV
LSS.CSNRTSK.R.ICP.TTSLARY.LAESNSS..RNTSSIYY.F.SI.SEIKRTDGKWL
FLRRFCTF.RSQG..SGVNEYSFCRI.W.FCELTST.NTDL.DAF.R.FLL.TK.YNS.R
PIGVQ.ISSF.KQQLYCLVNTISVLGLC.LCQKWWGVRISTGESKKNYFRNF.E.G.G.N
NSSFGKRCSE.SIFCHFSK.RWK.G.NHSPGNFLKKC.GYFCSSSRSKWKCYLAK.GFTI
LS.KFP..SKAK.WSLSYGCPSVEWFR.GWQSCSRWFLYLSFTLHTSSRRSK.SGVRL.S
SSKY.VTKSSFTSSV..N.SNIKLSHA.GK.LCSYISSTISFISCCKR.RIWR.DFLPLF
PYRSRR.SDTS.NS.DRRE.GCSRP.DLDTCCGR.SW.FRNGKIV.PLE.GSSIRERKRY
SNF.QFQIF..LEKRTYVYF.RRKSSKQESRRNSIS.AANYSYYSIIV.RNNSIRK.ESP
HFYKQ...QSS.DHIT.T.RGFC.PY

SEQ ID NO. 4414
STRAIN H36B
EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGVISKVDG
ERIKNTSSQLTFNQSFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQSHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYVTGNDGKAKINLKRVGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDSSQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFANLQALETPIYKTLSKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNNFKYFDNLKKEPMFISKEGKVVNKNLEEIALVKPQTTVTTQSLSKEITQSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT

SEQ ID NO. 4415
STRAIN 18RS21
EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGIISKVDG
ERIKNTSSQLTFNQSFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQSHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYITGNDGKAKINLKRMGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFANLQALETPIYKTISKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKEPMFISKKEKVVNKNLEEIILVKPQTTVTTQSLSKEITKSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT

SEQ ID NO. 4416
STRAIN M732
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSESK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTIKKNVEIF.FLTVNYLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPLNHKPC.ILIGRK.FFVIKKHKFDLLLMLVNLVRN.KNRWQMVI
S.KVLYVLKKPRIVIRS..VFLL.DLMVILRTYKHLKHRFIRRFLKVVSTINQMIQLIKT
NWSTMNQLLLKATTILPC.HNQRLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRIIHILPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIIVWMLFSGVV.IRMAKL.QMVFILIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELSLMKLIEH.A.PCLRKVVMFLHIVYN.FYLML.KMKNMGMRLLTIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4417
STRAIN COH1
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSESK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTIKKNVEIF.FLTVNYLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPLNHKPC.ILIGRK.FFVIKKHKFDLLLMLVNLVRN.KNRWQMVI
S.KVLYVLKKPRIVIRS..VFLL.DLMVILRTYKHLKHRFIRRFLKVVSTINQMIQLIKT
NWSTMNQLLLKATTILPC.HNQRLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRIIHILPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIIVWMLFSGVV.IRMAKL.QMVFILIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELSLMKLIEH.A.PCLRKVVMFLHIVYN.FYLML.KMKNMGMRLLTIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4418
STRAIN M781
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKSESK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG
NSKRPAINSLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAIIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQVLLVSLFLTIKKNVEIF.FLTVNYLWGLLVK.MA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SV.KILQVS.HLTRVLK.LIAKVAIVCWNNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQQHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPLNHKPC.ILIGRK.FFVIKKHKFDLLLMLVNLVRN.KNRWQMVI
S.KVLYVLKKPRIVIRS..VFLL.DLMVILRTYKHLKHRFIRRFLKVVSTINQMIQLIKT
NWSTMNQLLLKATTILPC.HNQRLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRIIHILPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIIVWMLFSGVV.IRMAKL.QMVFILIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELSLMKLIEH.A.PCLRKVVMFLHIVYN.FYLML.KMKNMGMRLLTIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419
STRAIN JM9130013
EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGIISKVDG
ERIKNTSSQLTFNQSFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQSHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYITGNDGKAKINLKRMGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFANLQALETPIYKTLSKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKEPMFISKKEKVVNKNLEEIILVKPQTTVTTQSLSKEITKSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT

SEQ ID NO. 4420
STRAIN 090
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGVISKVDG
ERIKNTSSQLTFNQSFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQSHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYVTGNDGKAKINLKRVGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFANLQALETPIYKTLSKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDAFQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKESMFISKEGKVVNKNLEEITLVKPQTTVTTQSLSKEITKSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT

SEQ ID NO. 4421
STRAIN CJB110
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGVISKVDG
ERIKNTSSQLTFNQSFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQNHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYVTGNDGKAKINLKRVGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFANLQALETPIYKTLSKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDAFQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESSYVPTYRLQLVLSHVVKDEEYGDETSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKESMFISKEGKVVNKNLEEITLVKPQTTVTTQSLSKEITKSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

STRAIN 1169NT

```
EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNMGADLEEEYPSKPETTNNKESNVVTNASTAIAQKVPSAYEEVKPKSK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDIFRLDSPKDDKHSFKNKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFLIPYRELPVGVISKVDG
ERIKNTSSQLTFNQRFEVVDSQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQ
YQTMSGTSMASPHVAGLMTMLQSHLAEKYKGMNLDSKKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVDAEKAIQAQYYVTGNDGKAKINLKRVGDKFDITVTIHKLVEGVKELY
YQANVATEQVNKGKFALKPQALLDTNWQKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFKEAKDSNQELMSIPFVGFNGDFASLQALETPIYKTLSKGSFYYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFENKVEDKT
IHLLERDAANNPYFAISPNKDGNRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
YRKNFHNNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKGSSYVPIYRLQLVLSHVVKDEEYGDETSYYYF
HIDQEGKATLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VISNSFKYFDNLKKEPMFISKKEKVVNKNLEEIILVKPHTTVTTQSLSKEITKSGNEKVL
TSTNNNSSRVAKIISPKHNGDSVNHT
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PRETTY of: /biotmp/msa209368.2{*}   February 10, 2003 02:09  ..

                             1                                                   50
      msa209368.2{147_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
      msa209368.2{147_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
      msa209368.2{147_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
    msa209368.2{147_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
      msa209368.2{147_2603}  vdkhhskkai lkltlittsi llmhsnqvna EEQELKNQEQ SPVIANVAQQ
  msa209368.2{147_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
       msa209368.2{147_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
    msa209368.2{147_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
    msa209368.2{147_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
      msa209368.2{147_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
      msa209368.2{147_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ EEQELKNQEQ SPVIANVAQQ
                  Consensus  ********** ********** ********** ********** **********

                             51                                                 100
      msa209368.2{147_COH1}  PSPSVTTNiV EKTSVTaASA SNTvKEMGDT SVKNDKTEDE LLEELSKNLD
      msa209368.2{147_M732}  PSPSVTTNiV EKTSVTaASA SNTvKEMGDT SVKNDKTEDE LLEELSKNLD
      msa209368.2{147_M781}  PSPSVTTNiV EKTSVTaASA SNTvKEMGDT SVKNDKTEDE LLEELSKNLD
    msa209368.2{147_18RS21}  PSPSVTTNtV EKTSVTaASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
      msa209368.2{147_2603}  PSPSVTTNtV EKTSVTaASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
  msa209368.2{147_JM9130013}  PSPSVTTNtV EKTSVTaASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
       msa209368.2{147_090}  PSPSVTTNiV EKTSVTaASA SNTvKEMGDT SVKNDKTEDE LLEELSKNLD
    msa209368.2{147_CJB110}  PSPSVTTNiV EKTSVTaASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
    msa209368.2{147_1169NT}  PSPSVTTNiV EKTSVTaASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
      msa209368.2{147_H36B}  PSPSVTTNtV EKTSVTsASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
      msa209368.2{147_A909}  PSPSVTTNtV EKTSVTsASA SNTaKEMGDT SVKNDKTEDE LLEELSKNLD
                  Consensus  ********_* ******_*** ***_****** ********** **********

                             101                                                150
      msa209368.2{147_COH1}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKseSK
      msa209368.2{147_M732}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKseSK
      msa209368.2{147_M781}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKseSK
    msa209368.2{147_18RS21}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
      msa209368.2{147_2603}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
  msa209368.2{147_JM9130013}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
       msa209368.2{147_090}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
    msa209368.2{147_CJB110}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
    msa209368.2{147_1169NT}  TSNmGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpkSK
      msa209368.2{147_H36B}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
      msa209368.2{147_A909}  TSNlGADLEE EYPSKPETTN NKESNVVTNA STAIAQKVPS AYEEVKpeSK
                  Consensus  ***_****** ********** ********** ********** ******__**

                             151                                                200
      msa209368.2{147_COH1}  SSLAVlDTSK ITKLQAtTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
      msa209368.2{147_M732}  SSLAVlDTSK ITKLQAtTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
      msa209368.2{147_M781}  SSLAVlDTSK ITKLQAtTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
    msa209368.2{147_18RS21}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
      msa209368.2{147_2603}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
  msa209368.2{147_JM9130013}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
       msa209368.2{147_090}  SSLAVfDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
    msa209368.2{147_CJB110}  SSLAVfDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
    msa209368.2{147_1169NT}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
      msa209368.2{147_H36B}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
      msa209368.2{147_A909}  SSLAVlDTSK ITKLQAiTQR GKGNVVAIID TGFDINHDIF RLDSPKDDKH
                  Consensus  *****_**** ******_*** ********** ********** **********

                             201                                                250
      msa209368.2{147_COH1}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
     msa209368.2{147_M732}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
     msa209368.2{147_M781}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
   msa209368.2{147_18RS21}  SFKtKtEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
     msa209368.2{147_2603}  SFKtKtEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
msa209368.2{147_JM9130013}  SFKtKtEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
      msa209368.2{147_090}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
   msa209368.2{147_CJB110}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
   msa209368.2{147_1169NT}  SFKnKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
     msa209368.2{147_H36B}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
     msa209368.2{147_A909}  SFKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANNTETV ADIAAAMKDG
                 Consensus  ***-*-**** ********** ********** ********** **********

                            251                                                300
     msa209368.2{147_COH1}  YGSEAKNIlH GTHVAGIFVG NSKRPAINsL LLEGAAPNAQ VLLMRIPDKI
     msa209368.2{147_M732}  YGSEAKNIlH GTHVAGIFVG NSKRPAINsL LLEGAAPNAQ VLLMRIPDKI
     msa209368.2{147_M781}  YGSEAKNIlH GTHVAGIFVG NSKRPAINsL LLEGAAPNAQ VLLMRIPDKI
   msa209368.2{147_18RS21}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
     msa209368.2{147_2603}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
msa209368.2{147_JM9130013}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
      msa209368.2{147_090}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
   msa209368.2{147_CJB110}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
   msa209368.2{147_1169NT}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
     msa209368.2{147_H36B}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
     msa209368.2{147_A909}  YGSEAKNIsH GTHVAGIFVG NSKRPAINgL LLEGAAPNAQ VLLMRIPDKI
                 Consensus  ********-* ********** ********-* ********** **********

                            301                                                350
     msa209368.2{147_COH1}  DSDKFGEAYA KAIiDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
     msa209368.2{147_M732}  DSDKFGEAYA KAIiDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
     msa209368.2{147_M781}  DSDKFGEAYA KAIiDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
   msa209368.2{147_18RS21}  DSDKFGEAYA KAItDAVNLG AKTINMSiGK TADSLIALND KVKLALKLAS
     msa209368.2{147_2603}  DSDKFGEAYA KAItDAVNLG AKTINMSiGK TADSLIALND KVKLALKLAS
msa209368.2{147_JM9130013}  DSDKFGEAYA KAItDAVNLG AKTINMSiGK TADSLIALND KVKLALKLAS
      msa209368.2{147_090}  DSDKFGEAYA KAItDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
   msa209368.2{147_CJB110}  DSDKFGEAYA KAItDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
   msa209368.2{147_1169NT}  DSDKFGEAYA KAItDAVNLG AKTINMSiGK TADSLIALND KVKLALKLAS
     msa209368.2{147_H36B}  DSDKFGEAYA KAItDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
     msa209368.2{147_A909}  DSDKFGEAYA KAItDAVNLG AKTINMSlGK TADSLIALND KVKLALKLAS
                 Consensus  ********** ***-****** *******-** ********** **********

                            351                                                400
     msa209368.2{147_COH1}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
     msa209368.2{147_M732}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
     msa209368.2{147_M781}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
   msa209368.2{147_18RS21}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
     msa209368.2{147_2603}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
msa209368.2{147_JM9130013}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
      msa209368.2{147_090}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
   msa209368.2{147_CJB110}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
   msa209368.2{147_1169NT}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
     msa209368.2{147_H36B}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
     msa209368.2{147_A909}  EKGVAVVVAA GNEGAFGMDY SKPLSTNPDY GTVNSPAISE DTLSVASYES
                 Consensus  ********** ********** ********** ********** **********

                            401                                                450
     msa209368.2{147_COH1}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKilkvrt
     msa209368.2{147_M732}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKilkvrt
     msa209368.2{147_M781}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKilkvrt
   msa209368.2{147_18RS21}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
     msa209368.2{147_2603}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
msa209368.2{147_JM9130013}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
      msa209368.2{147_090}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
   msa209368.2{147_CJB110}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
   msa209368.2{147_1169NT}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
     msa209368.2{147_H36B}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKdfegkd
     msa209368.2{147_A909}  LKTISEVVET TIEGKLVKLP IVTSKPFDKG KAYDVVYANY GAKKrl.r.g
                 Consensus  ********** ********** ********** ********** ****------

                            451                                                500
     msa209368.2{147_COH1}  lkvrlh.lsv vvdlil.lks lmlqmqvllv slfltikknv eiF.fltvny
     msa209368.2{147_M732}  lkvrlh.lsv vvdlil.lks lmlqmqvllv slfltikknv eiF.fltvny
     msa209368.2{147_M781}  lkvrlh.lsv vvdlil.lks lmlqmqvllv slfltikknv eiF.fltvny
   msa209368.2{147_18RS21}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
     msa209368.2{147_2603}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
msa209368.2{147_JM9130013}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
      msa209368.2{147_090}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
   msa209368.2{147_CJB110}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
   msa209368.2{147_1169NT}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
     msa209368.2{147_H36B}  fkgkialier gggldfmtki thatnagvvg ivifndqekr gnFlipyrel
     msa209368.2{147_A909}  l.r.dcin.a wwwt.fyd.n hscykcrccw yryf.rsrkt wkFsnslp.i
                 Consensus  ---------- ---------- ---------- ---------- --*-------

                            501                                                550
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
     msa209368.2{147_COH1}  lwGllvk.ma sv.Kilqvs. hltrvlk.li akvaivcwnn qvga.qlkeq
     msa209368.2{147_M732}  lwGllvk.ma sv.Kilqvs. hltrvlk.li akvaivcwnn qvga.qlkeq
     msa209368.2{147_M781}  lwGllvk.ma sv.Kilqvs. hltrvlk.li akvaivcwnn qvga.qlkeq
   msa209368.2{147_18RS21}  pvGiiskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
     msa209368.2{147_2603}  pvGiiskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
msa209368.2{147_JM9130013}  pvGiiskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
      msa209368.2{147_090}  pvGviskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
   msa209368.2{147_CJB110}  pvGviskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
   msa209368.2{147_1169NT}  pvGviskvdg eriKntssql tfnqrfevvd sqggnrmleq sswgvtaega
     msa209368.2{147_H36B}  pvGviskvdg eriKntssql tfnqsfevvd sqggnrmleq sswgvtaega
     msa209368.2{147_A909}  tcGgy..srw rayKkyfksv ni.pef.ss. .prwqsyagt iklgrds.rs
                 Consensus  --*------- ---*------ ---------- ---------- ----------

                            551                                                600
     msa209368.2{147_COH1}  sslm.qllal kfilqpiiin tkqclvqvwl hhmlqd..qc fkviwlrnik
     msa209368.2{147_M732}  sslm.qllal kfilqpiiin tkqclvqvwl hhmlqd..qc fkviwlrnik
     msa209368.2{147_M781}  sslm.qllal kfilqpiiin tkqclvqvwl hhmlqd..qc fkviwlrnik
   msa209368.2{147_18RS21}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
     msa209368.2{147_2603}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
msa209368.2{147_JM9130013}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
      msa209368.2{147_090}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
   msa209368.2{147_CJB110}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqnhlaekyk
   msa209368.2{147_1169NT}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
     msa209368.2{147_H36B}  ikpdvtasgf eiysstynnq yqtmsgtsma sphvaglmtm lqshlaekyk
     msa209368.2{147_A909}  nqa.cnsfwl .nlffnl..s ipnnvwykyg fttccrindn asksfg.ei.
                 Consensus  ---------- ---------- ---------- ---------- ----------

                            601                                                650
     msa209368.2{147_COH1}  g.i.ilknc. nclktss.aq qqhyivkrir rfihhvskvq v.lmlkKlsk
     msa209368.2{147_M732}  g.i.ilknc. nclktss.aq qqhyivkrir rfihhvskvq v.lmlkKlsk
     msa209368.2{147_M781}  g.i.ilknc. nclktss.aq qqhyivkrir rfihhvskvq v.lmlkKlsk
   msa209368.2{147_18RS21}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
     msa209368.2{147_2603}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
msa209368.2{147_JM9130013}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
      msa209368.2{147_090}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
   msa209368.2{147_CJB110}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
   msa209368.2{147_1169NT}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
     msa209368.2{147_H36B}  gmnldskkll elsknilmss atalyseedk afysprqqga gvvdaeKaiq
     msa209368.2{147_A909}  rdefrf.kia riv.khphel snsii..rg. gvlfttsarc rcs.c.Ksyp
                 Consensus  ---------- ---------- ---------- ---------- ------*---

                            651                                                700
     msa209368.2{147_COH1}  lnimlletma klklisnere inlisqlqfi nl.kvsknci iklm.qqnk.
     msa209368.2{147_M732}  lnimlletma klklisnere inlisqlqfi nl.kvsknci iklm.qqnk.
     msa209368.2{147_M781}  lnimlletma klklisnere inlisqlqfi nl.kvsknci iklm.qqnk.
   msa209368.2{147_18RS21}  aqyyitgndg kakinlkrmg dkfditvtih klvegvkely yqanvateqv
     msa209368.2{147_2603}  aqyyitgndg kakinlkrmg dkfditvtih klvegvkely yqanvateqv
msa209368.2{147_JM9130013}  aqyyitgndg kakinlkrmg dkfditvtih klvegvkely yqanvateqv
      msa209368.2{147_090}  aqyyvtgndg kakinlkrvg dkfditvtih klvegvkely yqanvateqv
   msa209368.2{147_CJB110}  aqyyvtgndg kakinlkrvg dkfditvtih klvegvkely yqanvateqv
   msa209368.2{147_1169NT}  aqyyvtgndg kakinlkrvg dkfditvtih klvegvkely yqanvateqv
     msa209368.2{147_H36B}  aqyyvtgndg kakinlkrvg dkfditvtih klvegvkely yqanvateqv
     msa209368.2{147_A909}  ssilcywkrw qs.n.sqtsg r.i.yhsyns .tcrrcqriv lss.csnrts
                 Consensus  ---------- ---------- ---------- ---------- ----------

                            701                                                750
     msa209368.2{147_COH1}  ikvnlplnhk pc.iligrk. ffvikkhkfd lllmlvnlvr n.Knrwqmvi
     msa209368.2{147_M732}  ikvnlplnhk pc.iligrk. ffvikkhkfd lllmlvnlvr n.Knrwqmvi
     msa209368.2{147_M781}  ikvnlplnhk pc.iligrk. ffvikkhkfd lllmlvnlvr n.Knrwqmvi
   msa209368.2{147_18RS21}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
     msa209368.2{147_2603}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
msa209368.2{147_JM9130013}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
      msa209368.2{147_090}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
   msa209368.2{147_CJB110}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
   msa209368.2{147_1169NT}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidasqfsq klKeqmangy
     msa209368.2{147_H36B}  nkgkfalkpq alldtnwqkv ilrdketqvr ftidssqfsq klKeqmangy
     msa209368.2{147_A909}  k.r.icp.tt slary.laes nss..rntss iyy.f.si.s eiKrtdgkwl
                 Consensus  ---------- ---------- ---------- ---------- --*-------

                            751                                                800
     msa209368.2{147_COH1}  s.kvlyvlkk privirs..v fll.dlmvil rtykhlkhrf irrflkvvst
     msa209368.2{147_M732}  s.kvlyvlkk privirs..v fll.dlmvil rtykhlkhrf irrflkvvst
     msa209368.2{147_M781}  s.kvlyvlkk privirs..v fll.dlmvil rtykhlkhrf irrflkvvst
   msa209368.2{147_18RS21}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktiskgsfy
     msa209368.2{147_2603}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktlskgsfy
msa209368.2{147_JM9130013}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktlskgsfy
      msa209368.2{147_090}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktlskgsfy
   msa209368.2{147_CJB110}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktlskgsfy
   msa209368.2{147_1169NT}  flegfvrfke akdsnqelms ipfvgfngdf aslqaletpi yktlskgsfy
     msa209368.2{147_H36B}  flegfvrfke akdsnqelms ipfvgfngdf anlqaletpi yktlskgsfy
     msa209368.2{147_A909}  flrrfctf.r sqg..sgvne ysfcri.w.f celtst.ntd l.daf.r.fl
                 Consensus  ---------- ---------- ---------- ---------- ----------
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
                           801                                                850
     msa209368.2{147_COH1} inqmiqlikt nwstmnqlll kattilpc.h nqrlgamlim skmvgs.n.h
     msa209368.2{147_M732} inqmiqlikt nwstmnqlll kattilpc.h nqrlgamlim skmvgs.n.h
     msa209368.2{147_M781} inqmiqlikt nwstmnqlll kattilpc.h nqrlgamlim skmvgs.n.h
   msa209368.2{147_18RS21} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
     msa209368.2{147_2603} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
msa209368.2{147_JM9130013} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
      msa209368.2{147_090} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
   msa209368.2{147_CJB110} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
   msa209368.2{147_1169NT} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
     msa209368.2{147_H36B} ykpndtthkd qleynesapf esnnytallt qsaswgyvdy vknggelela
     msa209368.2{147_A909} l.tk.yns.r pigvq.issf .kqqlyclvn tisvlglc.l cqkwwgvris
                 Consensus ---------- ---------- ---------- ---------- ----------

                           851                                                900
     msa209368.2{147_COH1} rrvqKelf.e llrirlrikq fifwkemqri ihilpflqik meigtkslpr
     msa209368.2{147_M732} rrvqKelf.e llrirlrikq fifwkemqri ihilpflqik meigtkslpr
     msa209368.2{147_M781} rrvqKelf.e llrirlrikq fifwkemqri ihilpflqik meigtkslpr
   msa209368.2{147_18RS21} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
     msa209368.2{147_2603} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
msa209368.2{147_JM9130013} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
      msa209368.2{147_090} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
   msa209368.2{147_CJB110} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
   msa209368.2{147_1169NT} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
     msa209368.2{147_H36B} pespKriilg tfenkvedkt ihllerdaan npyfaispnk dgnrdeitpq
     msa209368.2{147_A909} tgesKknyfr nf.e.g.g.n nssfgkrcse .sifchfsk. rwk.g.nhsp
                 Consensus ----*----- ---------- ---------- ---------- ----------

                           901                                                950
     msa209368.2{147_COH1} qls.emlrif llkf.ikmem lfgkvrfyhl ivkisiiiqs kvmviivwml
     msa209368.2{147_M732} qls.emlrif llkf.ikmem lfgkvrfyhl ivkisiiiqs kvmviivwml
     msa209368.2{147_M781} qls.emlrif llkf.ikmem lfgkvrfyhl ivkisiiiqs kvmviivwml
   msa209368.2{147_18RS21} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
     msa209368.2{147_2603} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
msa209368.2{147_JM9130013} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
      msa209368.2{147_090} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
   msa209368.2{147_CJB110} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
   msa209368.2{147_1169NT} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
     msa209368.2{147_H36B} atflrnvkdi saqvldqngn viwqskvlps yrknfhnnpk qsdghyrmda
     msa209368.2{147_A909} gnflkkc.gy fcsssrskwk cylak.gfti ls.kfp..sk ak.wslsygc
                 Consensus ---------- ---------- ---------- ---------- ----------

                           951                                               1000
     msa209368.2{147_COH1} fsgvv.irma kl.qmvFili ayvthq.qke qivrsqtlkf k.vlshqifl
     msa209368.2{147_M732} fsgvv.irma kl.qmvFili ayvthq.qke qivrsqtlkf k.vlshqifl
     msa209368.2{147_M781} fsgvv.irma kl.qmvFili ayvthq.qke qivrsqtlkf k.vlshqifl
   msa209368.2{147_18RS21} lqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
     msa209368.2{147_2603} lqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
msa209368.2{147_JM9130013} lqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
      msa209368.2{147_090} fqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
   msa209368.2{147_CJB110} fqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
   msa209368.2{147_1169NT} lqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
     msa209368.2{147_H36B} lqwsgldkdg kvvadgFyty rlrytpvaeg ansqesdfkv qvstkspnlp
     msa209368.2{147_A909} psvewfr.gw qscsrwFlyl sftlhtssrr sk.sgvrl.s ssky.vtkss
                 Consensus ---------- ------*--- ---------- ---------- ----------

                           1001                                              1050
     msa209368.2{147_COH1} helslmklie h.a.pclrkv vmflhivyn. fylml.Kmkn mgmrlltiis
     msa209368.2{147_M732} helslmklie h.a.pclrkv vmflhivyn. fylml.Kmkn mgmrlltiis
     msa209368.2{147_M781} helslmklie h.a.pclrkv vmflhivyn. fylml.Kmkn mgmrlltiis
   msa209368.2{147_18RS21} sraqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
     msa209368.2{147_2603} sraqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
msa209368.2{147_JM9130013} sraqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
      msa209368.2{147_090} llaqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
   msa209368.2{147_CJB110} llaqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
   msa209368.2{147_1169NT} sraqfdetnr tlslampkgs syvpiyrlql vlshvvKdee ygdetsyyyf
     msa209368.2{147_H36B} sraqfdetnr tlslampkes syvptyrlql vlshvvKdee ygdetsyhyf
     msa209368.2{147_A909} ftssv..n.s niklsha.gk .lcsyissti sfisccKr.r iwr.dflplf
                 Consensus ---------- ---------- ---------- ------*--- ----------

                           1051                                              1100
     msa209368.2{147_COH1} i.ikkvk.hf lkrlr.ervr lr.tlrp.hl lwkiklvilq r.nclts.ir
     msa209368.2{147_M732} i.ikkvk.hf lkrlr.ervr lr.tlrp.hl lwkiklvilq r.nclts.ir
     msa209368.2{147_M781} i.ikkvk.hf lkrlr.ervr lr.tlrp.hl lwkiklvilq r.nclts.ir
   msa209368.2{147_18RS21} hidqegkvtl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
     msa209368.2{147_2603} hidqegkvtl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
msa209368.2{147_JM9130013} hidqegkvtl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
      msa209368.2{147_090} hidqegkvtl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
   msa209368.2{147_CJB110} hidqegkvtl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
   msa209368.2{147_1169NT} hidqegkatl pktvkigese vavdpkaltl vvedkagnfa tvklsdllnk
     msa209368.2{147_H36B} hidqegkvtl pktvkigese vavdpktltl vvedkagnfa tvklsdllnk
     msa209368.2{147_A909} pyrsrr.sdt s.ns.drre. gcsrp.dldt ccgr.sw.fr ngkiv.ple.
                 Consensus ---------- ---------- ---------- ---------- ----------
```

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

```
                           1101                                               1150
    msa209368.2{147_COH1}  q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl
    msa209368.2{147_M732}  q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl
    msa209368.2{147_M781}  q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl
   msa209368.2{147_18RS21} avvsekenai visnsfkyfd nlkKepmfis kkeKvvnknl eeiilvkpqt
    msa209368.2{147_2603}  avvsekenai visnsfkyfd nlkKepmfis kkeKvvnknl eeiilvkpqt
msa209368.2{147_JM9130013} avvsekenai visnsfkyfd nlkKepmfis kkeKvvnknl eeiilvkpqt
     msa209368.2{147_090}  avvsekenai visnsfkyfd nlkKesmfis kegKvvnknl eeitlvkpqt
   msa209368.2{147_CJB110} avvsekenai visnsfkyfd nlkKesmfis kegKvvnknl eeitlvkpqt
   msa209368.2{147_1169NT} avvsekenai visnsfkyfd nlkKepmfis kkeKvvnknl eeiilvkpht
    msa209368.2{147_H36B}  avvsekenai visnnfkyfd nlkKepmfis kegKvvnknl eeialvkpqt
    msa209368.2{147_A909}  gssirerkry snf.qfqif. .leKrtyvyf .rrKsskqes rrnsis.aan
               Consensus   ---------- ---------- ---*------ ---*------ ----------

                           1151                                               1200
    msa209368.2{147_COH1}  qlllnhclkk .lnqemrkss llqtiivae. lrsyhlnitg illti~~~~~
    msa209368.2{147_M732}  qlllnhclkk .lnqemrkss llqtiivae. lrsyhlnitg illti~~~~~
    msa209368.2{147_M781}  qlllnhclkk .lnqemrkss llqtiivae. lrsyhlnitg illti~~~~~
   msa209368.2{147_18RS21} tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
    msa209368.2{147_2603}  tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhTlpst
msa209368.2{147_JM9130013} tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
     msa209368.2{147_090}  tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
   msa209368.2{147_CJB110} tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
   msa209368.2{147_1169NT} tvttqslske itksgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
    msa209368.2{147_H36B}  tvttqslske itqsgnekvl tstnnnssrv akiispkhng dsvnhT~~~~
    msa209368.2{147_A909}  ysyysiiv.r nnsirk.esp hfykq...qs s.dhit.t.r gfc.py~~~~
               Consensus   ---------- ---------- ---------- ---------- -----*****

                           1201                            1233
    msa209368.2{147_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
    msa209368.2{147_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
    msa209368.2{147_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
   msa209368.2{147_18RS21} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
    msa209368.2{147_2603}  sdratnglfv gtlallssll lylkpkktkn nsk
msa209368.2{147_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
     msa209368.2{147_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
   msa209368.2{147_CJB110} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
   msa209368.2{147_1169NT} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
    msa209368.2{147_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
    msa209368.2{147_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~
               Consensus   ********** ********** ********** ***
```

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

SEQ ID NO. 4501
STRAIN 2603
ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTTAGGATTGGTACAA
TTAGCGTTTTTTTCGGTAGCCAGTGTAAATGCTGATACCCCTAATCAACTAACAATCACA
CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG
ACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATAGCGAATTGAACCAGAAG
TATAAGAGTATCTTGACTTCTCCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA
AATGGTTCGTACTTTGGTCGTGCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCT
TTTTATATTGAATTACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGA
AAAGTTGAAACAGGCCGATTAAAACTTATTAAATATACAAAAGAAGGAAAGATAAAGAAA
AGGCTATCCGGAGTAATATTTGTATTATACGATAACCAGAATCAGCCAGTTCGCTTTAAA
AATGGACGATTTACGACCGATCAAGATGGGATTACTTCATTAGTAACTGATGATAAGGGA
GAAATTGAGGTTGAAGGTTTATTACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTA
ACTGGTTACCGTATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAG
GAAGTAGAGGTAGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAACCATCACAA
CCGCTTTTTCCACAATCATTTCTTCCTAAAACAGGAATGATTATTGGTGGAGGACTGACA
ATTCTTGGTTGTATTATTTTGGGAATTTTGTTTATCTTTTTAAGAAAAACTAAAAATAGC
AAATCTGAAAGAAACGATACAGTA

SEQ ID NO. 4502
STRAIN 090
GATACCCCTAATCAACTAACAATCACAC
AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTA
TGGACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGA
TAGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATA
CTAATGGtCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGT
GCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTTATATTGA
ATTACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAA
AAGTTGAAACAGGCCGATTAAAACTTATTAAATATACAAAAGAAGGAAAG
ATAAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAGAA
TCAGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGA
TTACTTCATTAGTAACTGATGATAAGGGAGAAATTGAGGTTGAAGGTTTA
TTACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGtTACCG
TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGG
AAGTaGAGGTaGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAA
CCATCACAACCG

SEQ ID NO. 4503
STRAIN H36B
GATACCCCTAATCAACTAACAATCACACAGA
TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG
ACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATAG
CGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACTA
ATGGtCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTGCT
TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTTATATTGAATT
ACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAAG
TTGAAACAGGCCGATTAAAACTTATTAAATATACAAAAGAAGGAAAGATA
AAGAAAAGGCTwTCCGGAGTAATATTTGTATTATACGATAACCAGAATCA
GCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATTA
CTTCATTAGTAACTGATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA
CCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT
ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG
TAGAGGTAGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAACCA
TCACAACCGC

SEQ ID NO. 4504
STRAIN 18RS21
GATACCCCTAATCAACTAACAATCACACAG
ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
GACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATA
GCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
AATGGtCAGACAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTGC
TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTTATATTGAAT
TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA
GTTGAAACAGGCCGATTAAAACTTATTAAATATACAAAAGAAGGAAAGAT
AAAGAAAAGGCTATCCGGAGTAATATTTGTATTATACGATAACCAGAATC
AGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATT
ACTTCATTAGTAACTGATGATAAGGGAGAAATTGAGGTTGAAGGTTTATT
ACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAA
GTAGAGGTAGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAACC
ATCACAACC

SEQ ID NO. 4505
STRAIN CJB110
GATACCCCTAATCAACTAACAATCACACA
GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT
GGaCTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGAT
AGCGAATTgAACCAGAAGTATAAGAGTATCTTGACTTCTCctACTGATAc
TAATGGTCAGACAAAGATAGCACTCCCAAATGGTTcGTACTTTGGTCGTG
CTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTTATATTGAA
TTACCAGATGATAAGTTATCAAATCAATTACAGatAAATCCTAAGCGAAA
AGTTGAAACAGGCCGATTaaAACTTATTAAATATACAAAAGAAGGAAAGA

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCAGAAT
CAGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGAT
TACTTCATTAGTAACTGATGATAAGGGAGAAATTGAGGTTGAAGGTTTAT
TACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTaCCGT
ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA
AGTAGAGGTAGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAAC
CATCACAACC

SEQ ID NO. 4506
STRAIN 1169NT
GATACCCCTAATCAACTAACAATCACACAG
ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
GACTGTGACTGACAACTTAAAAGTTGATTTATTGAGCCAAATGACAGATA
GCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
AATGGtCAgaCAAAGATAGCACTCCCAAATGGTTCGTACTTTGGTCGTGC
TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTTATATTGAAT
TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA
GTTGAAACAGGCCGATTAAAACTTATTAAATATACAAAAGAAGGAAAGAT
AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAGAATC
AGCCAGTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATT
ACTTCATTAGTAACtgaTGATAAGGGAGAAATTGAGGTTGAAGGTTTATT
ACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAA
GTAGAGGTAGAAAACGAAAAAGAAACTCCTCCACCAACAAATCCTAAACC
ATCACAACC

```
PRETTY of: /biotmp/msa184750.2{*}   May 13, 2003 06:23  ..

                           1                                                    50
   msa184750.2{150_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa184750.2{150_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa184750.2{150_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa184750.2{150_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa184750.2{150_2603}   atgaaaaaga ttagaaaaag tttaggactt ctactatgtt gctttttagg
   msa184750.2{150_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus   ********** ********** ********** ********** **********

                           51                                                  100
   msa184750.2{150_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GATACCC
 msa184750.2{150_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GATACCC
 msa184750.2{150_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GATACCC
 msa184750.2{150_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GATACCC
   msa184750.2{150_2603}   attggtacaa ttagcgtttt tttcggtagc cagtgtaaat gctGATACCC
   msa184750.2{150_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GATACCC
               Consensus   ********** ********** ********** ********** **********

                           101                                                 150
   msa184750.2{150_090}    CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
 msa184750.2{150_1169NT}   CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
 msa184750.2{150_CJB110}   CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
 msa184750.2{150_18RS21}   CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
   msa184750.2{150_2603}   CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
   msa184750.2{150_H36B}   CTAATCAACT AACAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
               Consensus   ********** ********** ********** ********** **********

                           151                                                 200
   msa184750.2{150_090}    GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
 msa184750.2{150_1169NT}   GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
 msa184750.2{150_CJB110}   GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
 msa184750.2{150_18RS21}   GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
   msa184750.2{150_2603}   GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
   msa184750.2{150_H36B}   GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAACT TAAAAGTTGA
               Consensus   ********** ********** ********** ********** **********

                           201                                                 250
   msa184750.2{150_090}    TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
 msa184750.2{150_1169NT}   TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
 msa184750.2{150_CJB110}   TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
 msa184750.2{150_18RS21}   TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
   msa184750.2{150_2603}   TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
   msa184750.2{150_H36B}   TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
               Consensus   ********** ********** ********** ********** **********

                           251                                                 300
   msa184750.2{150_090}    TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
 msa184750.2{150_1169NT}   TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
 msa184750.2{150_CJB110}   TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
 msa184750.2{150_18RS21}   TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
   msa184750.2{150_2603}   TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
   msa184750.2{150_H36B}   TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
               Consensus   ********** ********** ********** ********** **********

                           301                                                 350
```

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

```
    msa184750.2{150_090}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
 msa184750.2{150_1169NT}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
 msa184750.2{150_CJB110}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
 msa184750.2{150_18RS21}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
   msa184750.2{150_2603}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
   msa184750.2{150_H36B}  AATGGTTCGT ACTTTGGTCG TGCTTATAAA GCTGATCAAA GCGTTTCAAC
               Consensus  ********** ********** ********** ********** **********

                          351                                                400
    msa184750.2{150_090}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
 msa184750.2{150_1169NT}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
 msa184750.2{150_CJB110}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
 msa184750.2{150_18RS21}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
   msa184750.2{150_2603}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
   msa184750.2{150_H36B}  AATAGTACCT TTTTATATTG AATTACCAGA TGATAAGTTA TCAAATCAAT
               Consensus  ********** ********** ********** ********** **********

                          401                                                450
    msa184750.2{150_090}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
 msa184750.2{150_1169NT}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
 msa184750.2{150_CJB110}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
 msa184750.2{150_18RS21}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
   msa184750.2{150_2603}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
   msa184750.2{150_H36B}  TACAGATAAA TCCTAAGCGA AAAGTTGAAA CAGGCCGATT AAAACTTATT
               Consensus  ********** ********** ********** ********** **********

                          451                                                500
    msa184750.2{150_090}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTaTCaG GAGTAATATT
 msa184750.2{150_1169NT}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTaTCaG GAGTAATATT
 msa184750.2{150_CJB110}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTaTCaG GAGTAATATT
 msa184750.2{150_18RS21}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTaTCcG GAGTAATATT
   msa184750.2{150_2603}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTaTCcG GAGTAATATT
   msa184750.2{150_H36B}  AAATATACAA AAGAAGGAAA GATAAAGAAA AGGCTwTCcG GAGTAATATT
               Consensus  ********** ********** ********** *****_**_* **********

                          501                                                550
    msa184750.2{150_090}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
 msa184750.2{150_1169NT}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
 msa184750.2{150_CJB110}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
 msa184750.2{150_18RS21}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
   msa184750.2{150_2603}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
   msa184750.2{150_H36B}  TGTATTATAC GATAACCAGA ATCAGCCAGT TCGCTTTAAA AATGGACGAT
               Consensus  ********** ********** ********** ********** **********

                          551                                                600
    msa184750.2{150_090}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
 msa184750.2{150_1169NT}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
 msa184750.2{150_CJB110}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
 msa184750.2{150_18RS21}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
   msa184750.2{150_2603}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
   msa184750.2{150_H36B}  TTACGACCGA TCAAGATGGG ATTACTTCAT TAGTAACTGA TGATAAGGGA
               Consensus  ********** ********** ********** ********** **********

                          601                                                650
    msa184750.2{150_090}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
 msa184750.2{150_1169NT}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
 msa184750.2{150_CJB110}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
 msa184750.2{150_18RS21}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
   msa184750.2{150_2603}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
   msa184750.2{150_H36B}  GAAATTGAGG TTGAAGGTTT ATTACCTGGT AAGTATATTT TTCGAGAAGC
               Consensus  ********** ********** ********** ********** **********

                          651                                                700
    msa184750.2{150_090}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
 msa184750.2{150_1169NT}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
 msa184750.2{150_CJB110}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
 msa184750.2{150_18RS21}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
   msa184750.2{150_2603}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
   msa184750.2{150_H36B}  AAAAGCACTA ACTGGTTACC GTATATCTAT GAAGGATGCT GTAGTTGCTG
               Consensus  ********** ********** ********** ********** **********

                          701                                                750
    msa184750.2{150_090}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
 msa184750.2{150_1169NT}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
 msa184750.2{150_CJB110}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
 msa184750.2{150_18RS21}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
   msa184750.2{150_2603}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
   msa184750.2{150_H36B}  TAGTTGCTAA TAAAACACAG GAAGTAGAGG TAGAAAACGA AAAAGAAACT
               Consensus  ********** ********** ********** ********** **********

                          751                                                800
    msa184750.2{150_090}  CCTCCACCAA CAAATCCTAA ACCATCACAA CCg~~~~~~~ ~~~~~~~~~~
 msa184750.2{150_1169NT}  CCTCCACCAA CAAATCCTAA ACCATCACAA CC~~~~~~~~ ~~~~~~~~~~
```

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

```
msa184750.2{150_CJB110}  CCTCCACCAA CAAATCCTAA ACCATCACAA CC~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_18RS21}  CCTCCACCAA CAAATCCTAA ACCATCACAA CC~~~~~~~~ ~~~~~~~~~~
  msa184750.2{150_2603}  CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
  msa184750.2{150_H36B}  CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC~~~~~~ ~~~~~~~~~~
              Consensus  ********** ********** ********** **-******* **********

                         801                                                850
   msa184750.2{150_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa184750.2{150_2603}  tcttcctaaa acaggaatga ttattggtgg aggactgaca attcttggtt
  msa184750.2{150_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
              Consensus  ********** ********** ********** ********** **********

                         851                                                900
   msa184750.2{150_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184750.2{150_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa184750.2{150_2603}  gtattatttt gggaattttg tttatctttt taagaaaaac taaaaatagc
  msa184750.2{150_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
              Consensus  ********** ********** ********** ********** **********

                         901                   924
   msa184750.2{150_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
msa184750.2{150_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
msa184750.2{150_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
msa184750.2{150_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
  msa184750.2{150_2603}  aaatctgaaa gaaacgatac agta
  msa184750.2{150_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
              Consensus  ********** ********** ****
```

SEQ ID NO. 4507
STRAIN 2603
MKKIRKSLGLLLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNTTEEGISYRLWTV
TDNLKVDLLSQMTDSELNQKYKSILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP
FYIELPDDKLSNQLQINPKRKVETGRLKLIKYTKEGKIKKRLSGVIFVLYDNQNQPVRFK
NGRFTTDQDGITSLVTDDKGEIEVEGLLPGKYIFREAKALTGYRISMKDAVVAVVANKTQ
EVEVENEKETPPPTNPKPSQPLFPQSFLPKTGMIIGGGLTILGCIILGILFIFLRKTKNS
KSERNDTV

SEQ ID NO. 4508
STRAIN 090
DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNQPVRFKNGRFTTDQDGITSLVTDDKGEIEVEGLLPGK
YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQP

SEQ ID NO. 4509
STRAIN H36B
DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNQPVRFKNGRFTTDQDGITSLVTDDKGEIEVEGLLPGK
YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQP

SEQ ID NO. 4510
STRAIN 18RS21
DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNQPVRFKNGRFTTDQDGITSLVTDDKGEIEVEGLLPGK
YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

SEQ ID NO. 4511
STRAIN 1169NT
DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNQPVRFKNGRFTTDQDGITSLVTDDKGEIEVEGLLPGK
YIFREAKALTGYRISMKDAVVAVVANKTQEVEVENEKETPPPTNPKPSQ

```
PRETTY of: /biotmp/msa184868.2{*}   May 13, 2003 06:25  ..

                         1                                                   50
   msa184868.2{150_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~DTPNQLTIT QIGLQPNTTE
  msa184868.2{150_2603}  mkkirkslgl llccflglvq laffsvasvn aDTPNQLTIT QIGLQPNTTE
  msa184868.2{150_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~DTPNQLTIT QIGLQPNTTE
msa184868.2{150_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~DTPNQLTIT QIGLQPNTTE
msa184868.2{150_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~DTPNQLTIT QIGLQPNTTE
              Consensus  ********** ********** ********** ********** **********

                         51                                                 100
   msa184868.2{150_090}  EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
```

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

```
  msa184868.2{150_2603}  EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
  msa184868.2{150_H36B}  EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_1169NT}  EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_18RS21}  EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
              Consensus  ********** ********** ********** ********** **********

                         101                                                150
   msa184868.2{150_090}  NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVETGRLKLI
  msa184868.2{150_2603}  NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVETGRLKLI
  msa184868.2{150_H36B}  NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVETGRLKLI
msa184868.2{150_1169NT}  NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVETGRLKLI
msa184868.2{150_18RS21}  NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVETGRLKLI
              Consensus  ********** ********** ********** ********** **********

                         151                                                200
   msa184868.2{150_090}  KYTKEGKIKK RLSGVIFVLY DNQNQPVRFK NGRFTTDQDG ITSLVTDDKG
  msa184868.2{150_2603}  KYTKEGKIKK RLSGVIFVLY DNQNQPVRFK NGRFTTDQDG ITSLVTDDKG
  msa184868.2{150_H36B}  KYTKEGKIKK RLSGVIFVLY DNQNQPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_1169NT}  KYTKEGKIKK RLSGVIFVLY DNQNQPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_18RS21}  KYTKEGKIKK RLSGVIFVLY DNQNQPVRFK NGRFTTDQDG ITSLVTDDKG
              Consensus  ********** ********** ********** ********** **********

                         201                                                250
   msa184868.2{150_090}  EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
  msa184868.2{150_2603}  EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
  msa184868.2{150_H36B}  EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_1169NT}  EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_18RS21}  EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
              Consensus  ********** ********** ********** ********** **********

                         251                                                300
   msa184868.2{150_090}  PPPTNPKPSQ p~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa184868.2{150_2603}  PPPTNPKPSQ plfpqsflpk tgmiiggglt ilgciilgil fiflrktkns
  msa184868.2{150_H36B}  PPPTNPKPSQ p~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184868.2{150_1169NT}  PPPTNPKPSQ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa184868.2{150_18RS21}  PPPTNPKPSQ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
              Consensus  ********** -********* ********** ********** **********

                         301
   msa184868.2{150_090}  ~~~~~~~~
  msa184868.2{150_2603}  kserndtv
  msa184868.2{150_H36B}  ~~~~~~~~
msa184868.2{150_1169NT}  ~~~~~~~~
msa184868.2{150_18RS21}  ~~~~~~~~
              Consensus  ********
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

SEQ ID NO. 4601
STRAIN A909
TGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCAGGTGTAACTATATTACCTTT
CTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATGCTTTTCGTCCAGA
TAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA
ATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTGGGGCACATGGAAA
AACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATTACAGACACTTCTTTCCT
AATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTGTGTTTGAAGCTGA
TGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTATTACCAATATTGA
TTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATGCCTTTAATGACTA
TGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAAAACTTCATGAAAT
CACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCAAATGATTTTATAGCAAA
AGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTCTATAACCAAGAAGAAAT
TGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT
TGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGCATTTGAAGACATT
TTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTGTCATTATTGATGA
CTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTCGACAAAAATACCC
GTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACTCGTACGATAGCTCTTTT
AGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTATCTCGCTCAAATATATGG
TTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTTAGCTGCTAAGATTGT
CAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTACTCAATCATGATAATGC
TGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCTCTTTTGAAGAATT
ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602
STRAIN 1169NT
AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGC
AGGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGC
AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA
TCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGG
TGTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAA
TATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
CTCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGT
ATTCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGA
AGATCCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGA
TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
TTTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATAT
CTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT
AGCTGAGCATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGA
CGATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA
TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTT
CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGT
TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
AGATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC
TTTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTA
TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603
STRAIN 090
AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
ATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTA
TTCAATGCTTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA
GATTCAAAACTTCATGAAATCACTTCTAAGGCACCAATATATTATTATGGTTTTGAAGAT
TCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAGATTATTGAC
GATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTC
ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
TATCTTGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
GATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604
STRAIN H36B
AAAAGCAGGCTCTAGTgACGTTgACAAATATtATTTTACTCAACGTGGTTtAGAGCAAGCAGGT
ATAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGA
AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT
TTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTA
GCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATT
ACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTAC
TTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCA
ATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTC
AATGCTTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGAT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

CCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCA
AATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTC
TATAACCAAGAAGAAATTGGTCAGTTTCACGTACCAGCATACGGTAAACATAATATCTTA
AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT
GAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAAATTATTGACGAT
ACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCT
GCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACT
CGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTAT
CTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGAT
TTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTA
CTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAG
CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605
STRAIN 18RS21
AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
ATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTA
TTCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA
GATCCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGAT
TCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTTGAAGACGTTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGAC
GATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTC
ACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTT
TATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
GATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606
STRAIN M732
AAAAGCAGGCTCTAGTGACGTtGACAAATAtTATTTTACCCAACGTGGTTTAGAGCAAGCAG
GTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAG
GAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTG
TAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATA
TTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATT
ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT
CAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTAT
TCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAG
ATCCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATT
CAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTT
TCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATCT
TAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG
CTGAGCATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACG
ATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATG
CTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCA
CTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTT
ATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAgGTAGAAG
ATTTAGCTGCTAAgATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTT
TACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATG
AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607
STRAIN M781
AAAGCAGGCTCTAGTGACGTtGACAAATATTATTTTACCCAACGTGGTTTAGAGCAAGCAG
GTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAG
GAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAA
TATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
CTCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGT
ATTCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGA
AGATCCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGA
TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
TTTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATAT
CTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT
AGCTGAGCATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGA
CGATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA
TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTT
CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGT
TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
AGATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC
TTTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTA

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608
STRAIN CJB110
AAAAAGCAGGCTCTAGTGACGTtGACAAATAtTATTTTACCCAACGTGGTTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
ATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTA
TTCAATGCTTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA
GATTCAAAACTTCATGAAATCACTTCTAAGGCACCAATATATTATTATGGTTTTGAAGAT
TCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAGATTATTGAC
GATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTC
ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
TATCTTGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
GATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609
STRAIN JM9130013 (reverse complement)
GTTCAAAAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTGGTTTAGA
GCAAGCAGGTATAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGAT
TATTGCAGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAA
GGGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAG
TCTAGGTGTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTT
AAAAAATATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAA
TGCTAATTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCC
AGAATACTCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGA
GGACGTATTCAATGCTTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTA
TGGAGAAGATCCAAAACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTT
TGAAGATTCAAATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTT
TAAGGTTTTCTATAACCAAGAAGAAATTGGTCAGTTTCACGTACCAGCATACGGTAAACA
TAATATCTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGC
ATTAGTAGCTGAGCATTTGAAGACATTTTCAGGGGTAAAACGTCGTTTTACTGAGAAAAT
TATTGACGATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGAC
ATTAGATGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCA
TACGTTCACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGA
TAGCGTTTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAA
GGTAGAAGATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGT
CTCGCCTTTACTCAATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCA
ATTGTATGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610
STRAIN COH1 reverse complement
CAGGCTCTAGTGACGTGACAAATATtATTTTACCCAACGTGGTTAGAGCAAGCAGGTGTAA
CTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATG
CTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTA
AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATTACAG
ACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG
TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA
TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATG
CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA
AACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCAAATG
ATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTCTATA
ACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATCTTAAATG
CAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
ATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTG
TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
GACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA
CGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTATCTCG
CTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTTAG
CTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTACTCA
ATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
CTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611
STRAIN 2603
atgtcaaaaacttatcattttattggtattaaaggatccggaatgagtgccctagcactg
atgcttcatcaaatgggacataacgtccaaggaagtgacgttgacaaatattattttacc
caacgtggtttagagcaagcaggtgtaactatattacctttctcaccgaataatatcagt
gaggatttagagattattgcaggaaatgcttttcgtccagataacaatgaagagttggct
tatgttattgaaaagggctatcaatttaaacgatatcatgaatttctcggagattttatg
cgtcagttcactagtctaggtgtagctggggcacatggaaaaacctcaacgacaggttta
ttagctcatgttttaaaaaatattacagacacttctttcctaattggagatggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
cgtggttctgctaatgctaattactttgtgtttgaagctgatgaatacgaacgtcatttt
atgccgtaccatccagaatactcaattattaccaatattgattttgaccatcctgattat
tttacaggcttagaggacgtattcaatgcctttaatgactatgctaagcaagttcaaaaa
ggtttattcatttatggagaagatccaaaacttcatgaaatcacttctgaggcaccaata
tattattatggttttgaagattcaaatgattttatagcaaaagacatcactcgaactgtt
aatggttctgactttaaggttttctataaccaagaagaaattggtcagtttcatgtacca
gcatacggtaaacataatatcttaaatgcaactgctgttattgctaacctttacataatg
ggaattgatatggcattagtagctgagcatttgaagacgttttcaggggtaaagcgtcgt
tttactgagaagattattgacgatactgtcattattgatgactttgctcaccatcctact
gagattattgcgacattagatgctgctcgacaaaaatacccgtcaaaagaaattgtagct
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ttgagtcaagcggatagcgtttatctcgctcaaatatatggttctgctagagaagtagat
aatggtgaggtgaaggtagaagatttagctgctaagattgtcaaacactcagatttagtg
acagtcgaaaatgtctcgcctttactcaatcatgataatgctgtctatgtctttatgggt
gctggagacattcaattgtatgagcgctcttttgaagaattattagctaacctaactaaa
aatacacaa
```

SEQ ID NO. 4612
STRAIN COH1 reverse complement

```
CAGGCTCTAGTGACGTtGACAAATAtTATTTTACCCAACGTGGtTTAGAGCAAGCAGGTGTAA
CTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATG
CTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTA
AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATTACAG
ACACTTCTTTCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG
TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA
TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTATTCAATG
CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA
AACTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTTGAAGATTCAAATG
ATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTCTATA
ACCAAGAAGAAATTGGTCAGTTTCATGTACCAGCATACGGTAAACATAATATCTTAAATG
CAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
ATTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTTACTGAGAAGATTATTGACGATACTG
TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
GACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA
CGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTATCTCG
CTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTTAG
CTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTACTCA
ATCATGATAATGCTGTCTATGTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
CTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA
```

```
PRETTY of: /biotmp/msa56524.2{*}   November 26, 2002 08:06  ..
PRETTY of: /biotmp/msa253045.2{*}   January 31, 2003 03:51  ..

                            1                                                   50
      msa253045.2{157_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa253045.2{157_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa253045.2{157_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa253045.2{157_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa253045.2{157_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_2603}  atgtcaaaaa cttatcattt tattggtatt aaaggatccg gaatgagtgc
                 Consensus  ********** ********** ********** ********** **********

                            51                                                 100
      msa253045.2{157_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~aaagcaggc tctagtgacg
   msa253045.2{157_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~A Aaaagcaggc tctagtgacg
     msa253045.2{157_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ Aaaagcaggc tctagtgacg
msa253045.2{157_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~GttcaA Aaaagcaggc tctagtgacg
   msa253045.2{157_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ Aaaagcaggc tctagtgacg
     msa253045.2{157_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa253045.2{157_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~caggc tctagtgacg
     msa253045.2{157_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ Aaaagcaggc tctagtgacg
     msa253045.2{157_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~aaagcaggc tctagtgacg
   msa253045.2{157_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~aaagcaggc tctagtgacg
     msa253045.2{157_2603}  cctagcactg atgcttcatc aaatGggacA taacgtccaa ggaagtgacg
                 Consensus  ********** ********** ********** *--------- ----------

                            101                                                150
      msa253045.2{157_090}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
   msa253045.2{157_CJB110}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
     msa253045.2{157_H36B}  tTGACAAATA TTATTTTACt CAACGTGGTT TAGAGCAAGC AGGTaTAACT
msa253045.2{157_JM9130013}  tTGACAAATA TTATTTTACt CAACGTGGTT TAGAGCAAGC AGGTaTAACT
   msa253045.2{157_1169NT}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
     msa253045.2{157_A909}  ~TGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
     msa253045.2{157_COH1}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
     msa253045.2{157_M732}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
     msa253045.2{157_M781}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
   msa253045.2{157_18RS21}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
    msa253045.2{157_2603}  tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
                Consensus  -********* *********- ********** ********** ****-*****

                           151                                                200
     msa253045.2{157_090}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
   msa253045.2{157_CJB110}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_H36B}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
msa253045.2{157_JM9130013}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
  msa253045.2{157_1169NT}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_A909}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_COH1}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_M732}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_M781}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
   msa253045.2{157_18RS21}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
    msa253045.2{157_2603}  ATATTACCTT TCTCACCGAA TAATATCAGT GAGGATTTAG AGATTATTGC
                Consensus  ********** ********** ********** ********** **********

                           201                                                250
     msa253045.2{157_090}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
   msa253045.2{157_CJB110}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_H36B}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
msa253045.2{157_JM9130013}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
  msa253045.2{157_1169NT}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_A909}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_COH1}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_M732}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_M781}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
   msa253045.2{157_18RS21}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
    msa253045.2{157_2603}  AGGAAATGCT TTTCGTCCAG ATAACAATGA AGAGTTGGCT TATGTTATTG
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
     msa253045.2{157_090}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
   msa253045.2{157_CJB110}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_H36B}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
msa253045.2{157_JM9130013}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
  msa253045.2{157_1169NT}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_A909}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_COH1}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_M732}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_M781}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
   msa253045.2{157_18RS21}  AAAAGGGCTA TCAtTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
    msa253045.2{157_2603}  AAAAGGGCTA TCAaTTTAAA CGATATCATG AATTTCTCGG AGATTTTATG
                Consensus  ********** ***-****** ********** ********** **********

                           301                                                350
     msa253045.2{157_090}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
   msa253045.2{157_CJB110}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_H36B}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
msa253045.2{157_JM9130013}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
  msa253045.2{157_1169NT}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_A909}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_COH1}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_M732}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_M781}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
   msa253045.2{157_18RS21}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
    msa253045.2{157_2603}  CGTCAGTTCA CTAGTCTAGG TGTAGCTGGG GCACATGGAA AAACCTCAAC
                Consensus  ********** ********** ********** ********** **********

                           351                                                400
     msa253045.2{157_090}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
   msa253045.2{157_CJB110}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_H36B}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
msa253045.2{157_JM9130013}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
  msa253045.2{157_1169NT}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_A909}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_COH1}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_M732}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_M781}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
   msa253045.2{157_18RS21}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
    msa253045.2{157_2603}  GACAGGTTTA TTAGCTCATG TTTTAAAAAA TATTACAGAC ACTTCTTTCC
                Consensus  ********** ********** ********** ********** **********

                           401                                                450
     msa253045.2{157_090}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
   msa253045.2{157_CJB110}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_H36B}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
msa253045.2{157_JM9130013}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
  msa253045.2{157_1169NT}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_A909}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_COH1}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_M732}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_M781}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
  msa253045.2{157_18RS21}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
    msa253045.2{157_2603}  TAATTGGAGA TGGTACAGGA CGTGGTTCTG CTAATGCTAA TTACTTTGTG
                Consensus  ********** ********** ********** ********** **********

                           451                                                500
     msa253045.2{157_090}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
  msa253045.2{157_CJB110}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_H36B}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
msa253045.2{157_JM9130013} TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
  msa253045.2{157_1169NT}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_A909}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_COH1}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_M732}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_M781}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
  msa253045.2{157_18RS21}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
    msa253045.2{157_2603}  TTTGAAGCTG ATGAATACGA ACGTCATTTT ATGCCGTACC ATCCAGAATA
                Consensus  ********** ********** ********** ********** **********

                           501                                                550
     msa253045.2{157_090}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
  msa253045.2{157_CJB110}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
    msa253045.2{157_H36B}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
msa253045.2{157_JM9130013} CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
  msa253045.2{157_1169NT}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
    msa253045.2{157_A909}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
    msa253045.2{157_COH1}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
    msa253045.2{157_M732}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
    msa253045.2{157_M781}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCc
  msa253045.2{157_18RS21}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCt
    msa253045.2{157_2603}  CTCAATTATT ACCAATATTG ATTTTGACCA TCCTGATTAT TTTACAGGCt
                Consensus  ********** ********** ********** ********** *********-

                           551                                                600
     msa253045.2{157_090}  TAGAGGACGT ATTCAATGCt TTTAATGACT ATGCTAAGCA AGTTCAAAAA
  msa253045.2{157_CJB110}  TAGAGGACGT ATTCAATGCt TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_H36B}  TAGAGGACGT ATTCAATGCt TTTAATGACT ATGCTAAGCA AGTTCAAAAA
msa253045.2{157_JM9130013} TAGAGGACGT ATTCAATGCt TTTAATGACT ATGCTAAGCA AGTTCAAAAA
  msa253045.2{157_1169NT}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_A909}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_COH1}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_M732}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_M781}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
  msa253045.2{157_18RS21}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
    msa253045.2{157_2603}  TAGAGGACGT ATTCAATGCc TTTAATGACT ATGCTAAGCA AGTTCAAAAA
                Consensus  ********** *********- ********** ********** **********

                           601                                                650
     msa253045.2{157_090}  GGTTTATTCA TTTATGGAGA AGATtCAAAA CTTCATGAAA TCACTTCTaA
  msa253045.2{157_CJB110}  GGTTTATTCA TTTATGGAGA AGATtCAAAA CTTCATGAAA TCACTTCTaA
    msa253045.2{157_H36B}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
msa253045.2{157_JM9130013} GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
  msa253045.2{157_1169NT}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
    msa253045.2{157_A909}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
    msa253045.2{157_COH1}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
    msa253045.2{157_M732}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
    msa253045.2{157_M781}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
  msa253045.2{157_18RS21}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
    msa253045.2{157_2603}  GGTTTATTCA TTTATGGAGA AGATcCAAAA CTTCATGAAA TCACTTCTgA
                Consensus  ********** ********** ****-***** ********** ********-*

                           651                                                700
     msa253045.2{157_090}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
  msa253045.2{157_CJB110}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_H36B}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
msa253045.2{157_JM9130013} GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
  msa253045.2{157_1169NT}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_A909}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_COH1}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_M732}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_M781}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
  msa253045.2{157_18RS21}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
    msa253045.2{157_2603}  GGCACCAATA TATTATTATG GTTTTGAAGA TTCAAATGAT TTTATAGCAA
                Consensus  ********** ********** ********** ********** **********

                           701                                                750
     msa253045.2{157_090}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
  msa253045.2{157_CJB110}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
    msa253045.2{157_H36B}  AAGAtATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
msa253045.2{157_JM9130013} AAGAtATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
  msa253045.2{157_1169NT}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
    msa253045.2{157_A909}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
    msa253045.2{157_COH1}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
    msa253045.2{157_M732}  AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
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Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
   msa253045.2{157_M781}   AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
 msa253045.2{157_18RS21}   AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
   msa253045.2{157_2603}   AAGAcATCAC TCGAACTGTT AATGGTTCTG ACTTTAAGGT TTTCTATAAC
               Consensus   ****-***** ********** ********** ********** **********

                           751                                                800
    msa253045.2{157_090}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
 msa253045.2{157_CJB110}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_H36B}   CAAGAAGAAA TTGGTCAGTT TCAcGTACCA GCATACGGTA AACATAATAT
msa253045.2{157_JM9130013} CAAGAAGAAA TTGGTCAGTT TCAcGTACCA GCATACGGTA AACATAATAT
 msa253045.2{157_1169NT}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_A909}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_COH1}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_M732}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_M781}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
 msa253045.2{157_18RS21}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
   msa253045.2{157_2603}   CAAGAAGAAA TTGGTCAGTT TCAtGTACCA GCATACGGTA AACATAATAT
               Consensus   ********** ********** ***-****** ********** **********

                           801                                                850
    msa253045.2{157_090}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
 msa253045.2{157_CJB110}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_H36B}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
msa253045.2{157_JM9130013} CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
 msa253045.2{157_1169NT}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_A909}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_COH1}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_M732}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_M781}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
 msa253045.2{157_18RS21}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
   msa253045.2{157_2603}   CTTAAATGCA ACTGCTGTTA TTGCTAACCT TTACATAATG GGAATTGATA
               Consensus   ********** ********** ********** ********** **********

                           851                                                900
    msa253045.2{157_090}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAaCGTCGT
 msa253045.2{157_CJB110}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAaCGTCGT
   msa253045.2{157_H36B}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAaCGTCGT
msa253045.2{157_JM9130013} TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAaCGTCGT
 msa253045.2{157_1169NT}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
   msa253045.2{157_A909}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
   msa253045.2{157_COH1}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
   msa253045.2{157_M732}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
   msa253045.2{157_M781}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
 msa253045.2{157_18RS21}   TGGCATTAGT AGCTGAGCAT TTGAAGACaT TTTCAGGGGT AAAgCGTCGT
   msa253045.2{157_2603}   TGGCATTAGT AGCTGAGCAT TTGAAGACgT TTTCAGGGGT AAAgCGTCGT
               Consensus   ********** ********** ********-* ********** ***-******

                           901                                                950
    msa253045.2{157_090}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
 msa253045.2{157_CJB110}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_H36B}   TTTACTGAGA AaATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
msa253045.2{157_JM9130013} TTTACTGAGA AaATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
 msa253045.2{157_1169NT}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_A909}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_COH1}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_M732}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_M781}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
 msa253045.2{157_18RS21}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
   msa253045.2{157_2603}   TTTACTGAGA AgATTATTGA CGATACTGTC ATTATTGATG ACTTTGCTCA
               Consensus   ********** *-******** ********** ********** **********

                           951                                               1000
    msa253045.2{157_090}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
 msa253045.2{157_CJB110}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_H36B}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
msa253045.2{157_JM9130013} CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
 msa253045.2{157_1169NT}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_A909}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_COH1}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_M732}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_M781}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
 msa253045.2{157_18RS21}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
   msa253045.2{157_2603}   CCATCCTACT GAGATTATTG CGACATTAGA TGCTGCTCGA CAAAAATACC
               Consensus   ********** ********** ********** ********** **********

                           1001                                              1050
    msa253045.2{157_090}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
 msa253045.2{157_CJB110}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
   msa253045.2{157_H36B}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
msa253045.2{157_JM9130013} CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
 msa253045.2{157_1169NT}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
   msa253045.2{157_A909}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
   msa253045.2{157_COH1}   CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
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Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
     msa253045.2{157_M732}  CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
     msa253045.2{157_M781}  CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
   msa253045.2{157_18RS21}  CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
     msa253045.2{157_2603}  CGTCAAAAGA AATTGTAGCT ATTTTCCAAC CGCATACGTT CACTCGTACG
                 Consensus  ********** ********** ********** ********** **********

                            1051                                              1100
      msa253045.2{157_090}  ATAGCTCTTT TAGACGAtTT TGCCCATGCt TTGAGTCAAG CGGATAGCGT
   msa253045.2{157_CJB110}  ATAGCTCTTT TAGACGAtTT TGCCCATGCt TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_H36B}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
msa253045.2{157_JM9130013}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
   msa253045.2{157_1169NT}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_A909}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_COH1}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_M732}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_M781}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
   msa253045.2{157_18RS21}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
     msa253045.2{157_2603}  ATAGCTCTTT TAGACGAaTT TGCCCATGCc TTGAGTCAAG CGGATAGCGT
                 Consensus  ********** *******_** *********_ ********** **********

                            1101                                              1150
      msa253045.2{157_090}  TTATCTtGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
   msa253045.2{157_CJB110}  TTATCTtGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_H36B}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
msa253045.2{157_JM9130013}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
   msa253045.2{157_1169NT}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_A909}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_COH1}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_M732}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_M781}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
   msa253045.2{157_18RS21}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
     msa253045.2{157_2603}  TTATCTcGCT CAAATATATG GTTCTGCTAG AGAAGTAGAT AATGGTGAGG
                 Consensus  ******_*** ********** ********** ********** **********

                            1151                                              1200
      msa253045.2{157_090}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
   msa253045.2{157_CJB110}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_H36B}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
msa253045.2{157_JM9130013}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
   msa253045.2{157_1169NT}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_A909}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_COH1}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_M732}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_M781}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
   msa253045.2{157_18RS21}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
     msa253045.2{157_2603}  TGAAGGTAGA AGATTTAGCT GCTAAGATTG TCAAACACTC AGATTTAGTG
                 Consensus  ********** ********** ********** ********** **********

                            1201                                              1250
      msa253045.2{157_090}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
   msa253045.2{157_CJB110}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_H36B}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
msa253045.2{157_JM9130013}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
   msa253045.2{157_1169NT}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_A909}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_COH1}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_M732}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_M781}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
   msa253045.2{157_18RS21}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
     msa253045.2{157_2603}  ACAGTCGAAA ATGTCTCGCC TTTACTCAAT CATGATAATG CTGTCTATGT
                 Consensus  ********** ********** ********** ********** **********

                            1251                                              1300
      msa253045.2{157_090}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
   msa253045.2{157_CJB110}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_H36B}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
msa253045.2{157_JM9130013}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
   msa253045.2{157_1169NT}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_A909}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_COH1}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_M732}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_M781}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
   msa253045.2{157_18RS21}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
     msa253045.2{157_2603}  CTTTATGGGT GCTGGAGACA TTCAATTGTA TGAGCGCTCT TTTGAAGAAT
                 Consensus  ********** ********** ********** ********** **********

                            1301                        1329
      msa253045.2{157_090}  TATTAGCTAA CCTAACTAAA AATACACAA
   msa253045.2{157_CJB110}  TATTAGCTAA CCTAACTAAA AATACACAA
     msa253045.2{157_H36B}  TATTAGCTAA CCTAACTAAA AATACACAA
msa253045.2{157_JM9130013}  TATTAGCTAA CCTAACTAAA AATACACAA
   msa253045.2{157_1169NT}  TATTAGCTAA CCTAACTAAA AATACACAA
     msa253045.2{157_A909}  TATTAGCTAA CCTAACTAAA AATACACAA
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
    msa253045.2{157_COH1}  TATTAGCTAA CCTAACTAAA AATACACAA
    msa253045.2{157_M732}  TATTAGCTAA CCTAACTAAA AATACACAA
    msa253045.2{157_M781}  TATTAGCTAA CCTAACTAAA AATACACAA
  msa253045.2{157_18RS21}  TATTAGCTAA CCTAACTAAA AATACACAA
    msa253045.2{157_2603}  TATTAGCTAA CCTAACTAAA AATACACAA
                Consensus  ********** ********** *********
```

SEQ ID NO. 4613
STRAIN A909 frame: 2

```
DKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHFKRYHE
FLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANANYFVFEAD
EYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEI
TSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVI
ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLDAARQKYP
SKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIV
KHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4614
STRAIN 1169NT frame: 2

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4615
STRAIN 090 FRAME:1

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DSKLHEITSKAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4616
STRAIN H36B frame: 2

```
KAGSSDVDKYYFTQRGLEQAGITILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4617
STRAIN 18RS21 frame: 1

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4618
STRAIN M732 frame: 2

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4619
STRAIN JM9130013 frame: 2

```
FKKAGSSDVDKYYFTQRGLEQAGITILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEK
GYHFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSAN
ANYFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIY
GEDPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKH
NILNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIAT
LDAARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVK
VEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4620
STRAIN M781 frame: 1

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4621
STRAIN CJB110 frame: 3

```
KAGSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
DSKLHEITSKAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNI
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLD
AARQKYPSKEIVAIFQPHTFTRTIALLDDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4622
STRAIN 2603 frame: 1

```
MSKTYHFIGIKGSGMSALALMLHQMGHNVQGSDVDKYYFTQRGLEQAGVTILPFSPNNIS
EDLEIIAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL
LAHVLKNITDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIITNIDFDHPDY
FTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEITSEAPIYYYGFEDSNDFIAKDITRTV
NGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVIANLYIMGIDMALVAEHLKTFSGVKRR
FTEKIIDDTVIIDDFAHHPTEIIATLDAARQKYPSKEIVAIFQPHTFTRTIALLDEFAHA
LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMG
AGDIQLYERSFEELLANLTKNTQ
```

SEQ ID NO. 4623
STRAIN COH1 frame: 3

```
GSSDVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHF
KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANANYF
VFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDP
KLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILN
ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIIATLDAA
RQKYPSKEIVAIFQPHTFTRTIALLDEFAHALSQADSVYLAQIYGSAREVDNGEVKVEDL
AAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ
```

```
PRETTY of: /biotmp/msa56635.2{*}   November 26, 2002 08:08  ..

                              1                                                    50
       msa253220.2{157_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
     msa253220.2{157_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
    msa253220.2{157_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
     msa253220.2{157_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
       msa253220.2{157_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
       msa253220.2{157_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGvT
       msa253220.2{157_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~g ssdvDKYYFT QRGLEQAGvT
       msa253220.2{157_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~kag ssdvDKYYFT QRGLEQAGiT
  msa253220.2{157_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~fkkag ssdvDKYYFT QRGLEQAGiT
       msa253220.2{157_2603}  msktyhfigi kgsgmsalal mlhqmghnvq gsdvDKYYFT QRGLEQAGvT
       msa253220.2{157_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~DKYYFT QRGLEQAGvT
                  Consensus   ********** ********** *******--- ---****** ********-*

                              51                                                  100
       msa253220.2{157_090}   ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
     msa253220.2{157_CJB110}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
    msa253220.2{157_1169NT}   ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
     msa253220.2{157_18RS21}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
       msa253220.2{157_M732}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
       msa253220.2{157_M781}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
       msa253220.2{157_COH1}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
       msa253220.2{157_H36B}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
  msa253220.2{157_JM9130013}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
       msa253220.2{157_2603}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYqFK RYHEFLGDFM
       msa253220.2{157_A909}  ILPFSPNNIS EDLEIIAGNA FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
                  Consensus   ********** ********** ********** *******-** **********

                              101                                                 150
       msa253220.2{157_090}   RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
     msa253220.2{157_CJB110}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
    msa253220.2{157_1169NT}   RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
     msa253220.2{157_18RS21}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_M732}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_M781}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_COH1}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_H36B}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
  msa253220.2{157_JM9130013}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_2603}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
       msa253220.2{157_A909}  RQFTSLGVAG AHGKTSTTGL LAHVLKNITD TSFLIGDGTG RGSANANYFV
                  Consensus   ********** ********** ********** ********** **********

                              151                                                 200
       msa253220.2{157_090}   FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
```

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

```
   msa253220.2{157_CJB110}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
   msa253220.2{157_1169NT}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
   msa253220.2{157_18RS21}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_M732}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_M781}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_COH1}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_H36B}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
msa253220.2{157_JM9130013}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_2603}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
     msa253220.2{157_A909}  FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDVFNA FNDYAKQVQK
                 Consensus  ********** ********** ********** ********** **********

                            201                                                250
      msa253220.2{157_090}  GLFIYGEDsK LHEITSkAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
   msa253220.2{157_CJB110}  GLFIYGEDsK LHEITSkAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
   msa253220.2{157_1169NT}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
   msa253220.2{157_18RS21}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_M732}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_M781}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_COH1}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_H36B}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
msa253220.2{157_JM9130013}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_2603}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
     msa253220.2{157_A909}  GLFIYGEDpK LHEITSeAPI YYYGFEDSND FIAKDITRTV NGSDFKVFYN
                 Consensus  ********_* ******_*** ********** ********** **********

                            251                                                300
      msa253220.2{157_090}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
   msa253220.2{157_CJB110}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
   msa253220.2{157_1169NT}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
   msa253220.2{157_18RS21}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_M732}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_M781}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_COH1}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_H36B}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
msa253220.2{157_JM9130013}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_2603}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
     msa253220.2{157_A909}  QEEIGQFHVP AYGKHNILNA TAVIANLYIM GIDMALVAEH LKTFSGVKRR
                 Consensus  ********** ********** ********** ********** **********

                            301                                                350
      msa253220.2{157_090}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
   msa253220.2{157_CJB110}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
   msa253220.2{157_1169NT}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
   msa253220.2{157_18RS21}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_M732}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_M781}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_COH1}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_H36B}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
msa253220.2{157_JM9130013}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_2603}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
     msa253220.2{157_A909}  FTEKIIDDTV IIDDFAHHPT EIIATLDAAR QKYPSKEIVA IFQPHTFTRT
                 Consensus  ********** ********** ********** ********** **********

                            351                                                400
      msa253220.2{157_090}  IALLDdFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
   msa253220.2{157_CJB110}  IALLDdFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
   msa253220.2{157_1169NT}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
   msa253220.2{157_18RS21}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_M732}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_M781}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_COH1}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_H36B}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
msa253220.2{157_JM9130013}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_2603}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
     msa253220.2{157_A909}  IALLDeFAHA LSQADSVYLA QIYGSAREVD NGEVKVEDLA AKIVKHSDLV
                 Consensus  *****_**** ********** ********** ********** **********

                            401                                         443
      msa253220.2{157_090}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
   msa253220.2{157_CJB110}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
   msa253220.2{157_1169NT}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
   msa253220.2{157_18RS21}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_M732}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_M781}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_COH1}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_H36B}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
msa253220.2{157_JM9130013}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_2603}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
     msa253220.2{157_A909}  TVENVSPLLN HDNAVYVFMG AGDIQLYERS FEELLANLTK NTQ
                 Consensus  ********** ********** ********** ********** ***
```

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

SEQ ID NO. 4701
STRAIN A909
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAA
GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4702
STRAIN H36B
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAA
GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4703
STRAIN 18RS21
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAA
GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4704
STRAIN M732
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAA
GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4705
STRAIN COH1
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT
TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAA
GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4706
STRAIN M781
TATTTTTTAACAACAAAAAAAGGAAAAGAGC
TAAGGAAAAATGCAGAAAAATTCTATGGAGAATATAAAGAAAATCCAGAA
GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC
TGTTGATACTTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGA
CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT
GACTTTGCTAATGATTTTGTCAATCAAGCTAAATCAAAATTCTCAGACGA
GGATACTGCTAAAAAAGAAGATAAGGCTCCTGAAACAAAAGTAGAAGATA
TTGTCATTGATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4707
STRAIN 2603
tattttttaacaacaaaaaaaggaaaagagctaaggaaaaatgcagaaaa
attctatggagaatataaagaaaatccagaagaatatcatcaaatagcta
aagataaagcaagtgaatattcaaatttagctgttgatacttttaaagat
tataaaggtaaatttgaatcaggtgaattgacaacagaggatatcgtctc
agccgttaaggaaaaaagcggagaagtagttgactttgctaatgattttg
tcaatcaagctaaatcaaaattctcagacgaggatactgctaaaaaagaa
gataaggctcctgaaacaaaagtagaagatattgtcattgattataaaga
aaacacagaagataaagaaaaa

SEQ ID NO. 4708
STRAIN 090
TATTTTTTaACaACAAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTTAAAGAT

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGCTAAAAAAGAa
GATAAGGCTCCTGAAACAAAaGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4709
STRAIN CJB110
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAAA
ATGCAGAAAAATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCAT
CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC
TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTgAATTGACAACAGAGG
ATATCGTCTCAGCCGtTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCT
AATGATTTTGTCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGC
TAAAAAAGAAGATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTG
ATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4710
STRAIN 1169NT
TATTTTTTAACAACAAAAAAAGGAAAAGAGCTAAGGAAA
AATGCAGAAAAATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCA
TCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA
CTTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAG
GATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGC
TAATGATTTTGTCAATCAAGCTAAATCAAAATTCTCAGATGAGGATACTG
CTAAAAAAGAAAATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATT
GATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4711
STRAIN JM9130013
TATTTTTTAaCAACAAAAAAAGGAAAAGAGCTAAGGAAAA
ATGCAGAAAAATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCAT
CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC
TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGG
ATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCT
AATGATTTTGTCAATCAAGCTAAATCAAAATTCTCAGACGAGGATACTGC
TAAAAAAGAAGATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTG
ATTATAAAGAAAACACAGAAGATAAAGAAAAA

```
PRETTY of: /biotmp/msa68511.2{*}   January 22, 2003 05:47  ..

                             1                                                   50
      msa68511.2{164_090}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
    msa68511.2{164_18RS21}  TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_2603}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_A909}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
    msa68511.2{164_CJB110}  TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_COH1}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_H36B}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
 msa68511.2{164_JM9130013}  TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_M732}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
     msa68511.2{164_M781}   TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
    msa68511.2{164_1169NT}  TATTTTTTAA CAACAAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
                Consensus   ********** ********** ********** ********** **********

                             51                                                 100
      msa68511.2{164_090}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
    msa68511.2{164_18RS21}  ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_2603}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_A909}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
    msa68511.2{164_CJB110}  ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_COH1}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_H36B}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
 msa68511.2{164_JM9130013}  ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_M732}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
     msa68511.2{164_M781}   ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
    msa68511.2{164_1169NT}  ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
                Consensus   ********** ********** ********** ********** **********

                             101                                                150
      msa68511.2{164_090}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
    msa68511.2{164_18RS21}  AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_2603}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_A909}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
    msa68511.2{164_CJB110}  AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_COH1}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_H36B}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
 msa68511.2{164_JM9130013}  AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_M732}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
     msa68511.2{164_M781}   AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
    msa68511.2{164_1169NT}  AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
                Consensus   ********** ********** ********** ********** **********
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Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

```
                           151                                                200
      msa68511.2{164_090}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
    msa68511.2{164_18RS21}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_2603}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_A909}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
   msa68511.2{164_CJB110}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_COH1}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_H36B}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
msa68511.2{164_JM9130013}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_M732}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
     msa68511.2{164_M781}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
   msa68511.2{164_1169NT}  TATAAAGGTA AATTTGAATC AGGTGAATTG ACAACAGAGG ATATCGTCTC
                Consensus  ********** ********** ********** ********** **********

                           201                                                250
      msa68511.2{164_090}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
   msa68511.2{164_18RS21}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_2603}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_A909}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
   msa68511.2{164_CJB110}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_COH1}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_H36B}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
msa68511.2{164_JM9130013}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_M732}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
     msa68511.2{164_M781}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
   msa68511.2{164_1169NT}  AGCCGTTAAG GAAAAAAGCG GAGAAGTAGT TGACTTTGCT AATGATTTTG
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
      msa68511.2{164_090}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
   msa68511.2{164_18RS21}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_2603}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_A909}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
   msa68511.2{164_CJB110}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_COH1}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_H36B}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
msa68511.2{164_JM9130013}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_M732}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
     msa68511.2{164_M781}  TCAATCAAGC TAAATCAAAA TTCTCAGAcG AGGATACTGC TAAAAAAGAA
   msa68511.2{164_1169NT}  TCAATCAAGC TAAATCAAAA TTCTCAGAtG AGGATACTGC TAAAAAAGAA
                Consensus  ********** ********** ********-* ********** **********

                           301                                                350
      msa68511.2{164_090}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
   msa68511.2{164_18RS21}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_2603}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_A909}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
   msa68511.2{164_CJB110}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_COH1}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_H36B}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
msa68511.2{164_JM9130013}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_M732}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
     msa68511.2{164_M781}  gATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
   msa68511.2{164_1169NT}  aATAAGGCTC CTGAAACAAA AGTAGAAGAT ATTGTCATTG ATTATAAAGA
                Consensus  -********* ********** ********** ********** **********

                           351                  372
      msa68511.2{164_090}  AAACACAGAA GATAAAGAAA AA
   msa68511.2{164_18RS21}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_2603}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_A909}  AAACACAGAA GATAAAGAAA AA
   msa68511.2{164_CJB110}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_COH1}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_H36B}  AAACACAGAA GATAAAGAAA AA
msa68511.2{164_JM9130013}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_M732}  AAACACAGAA GATAAAGAAA AA
     msa68511.2{164_M781}  AAACACAGAA GATAAAGAAA AA
   msa68511.2{164_1169NT}  AAACACAGAA GATAAAGAAA AA
                Consensus  ********** ********** **
```

SEQ ID NO. 4712
STRAIN 2603
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4713
STRAIN A909 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4715
STRAIN 18RS21 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4716
STRAIN M732 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4717
STRAIN _COH1 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4718
STRAIN _M781 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4719
STRAIN _090 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4720
STRAIN _CJB110 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4721
STRAIN 1169NT frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKENKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4722
STRAIN _JM9130013 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGKFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

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PRETTY of: /biotmp/msa68746.2{*}   January 22, 2003 05:54  ..

                                1                                                   50
       msa68746.2{164_090}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
    msa68746.2{164_1169NT}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
    msa68746.2{164_18RS21}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_2603}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_A909}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
    msa68746.2{164_CJB110}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_COH1}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_H36B}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
 msa68746.2{164_JM9130013}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_M732}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
      msa68746.2{164_M781}   YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
                 Consensus   ********** ********** ********** ********** **********

                                51                                                 100
       msa68746.2{164_090}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
    msa68746.2{164_1169NT}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
    msa68746.2{164_18RS21}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_2603}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_A909}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
    msa68746.2{164_CJB110}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_COH1}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_H36B}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
 msa68746.2{164_JM9130013}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_M732}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
      msa68746.2{164_M781}   YKGKFESGEL TTEDIVSAVK EKSGEVVDFA NDFVNQAKSK FSDEDTAKKE
```

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

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              Consensus   ********** ********** ********** ********** **********

                          101                   124
      msa68746.2{164_090}  dKAPETKVED IVIDYKENTE DKEK
   msa68746.2{164_1169NT}  nKAPETKVED IVIDYKENTE DKEK
   msa68746.2{164_18RS21}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_2603}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_A909}  dKAPETKVED IVIDYKENTE DKEK
   msa68746.2{164_CJB110}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_COH1}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_H36B}  dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_JM9130013}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_M732}  dKAPETKVED IVIDYKENTE DKEK
     msa68746.2{164_M781}  dKAPETKVED IVIDYKENTE DKEK
                Consensus  -********* ********** ****
```

Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801
STRAIN 2603
aatagtactgagacaagtgcttcagtagttcctactacaaatactatcgt
tcaaactaatgacagtaatcctaccgcaaaatttgtatcagaatcaggac
aatctgtaataggtcaagtaaaaccagataattctgcggcgcttacaaca
gttgacacgcctcatcatatttcagctccagatgctttaaaaacaactca
atcaagtcctgtcgttgagagtacttctactaagttaactgaagagactt
acaaacaaaaagatggtcaagatttagccaacatggtgagaagtggtcaa
gttactagtgaggaactcgttaatatggcatacgatattattgctaaaga
aaacccatctttaaatgcagtcattactactagacgccaagaagctattg
aagaggctagaaaacttaaagataccaatcagccgtttttaggtgttccc
ttgttagtcaaggggttagggcacagtattaaaggtggtgaaaccaataa
tggcttgatctatgcagatggaaaaattagcacatttgacagtagctatg
tcaaaaaatataaagatttaggatttattattttaggacaaacgaacttt
ccagagtatgggtggcgtaatataacagattctaaattatacggtctaac
gcataatccttgggatcttgctcataatgctggtggctcttctggtggaa
gtgcagcagccattgctagcggaatgacgccaattgctagcggtagtgat
gctggtggttctatccgtattccatcttcttggacgggcttggtaggttt
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cagcagttcattttccattaactaagtcatctagagacgcagaaacatta
ttaacttatctaaagaaaagcgatcaaacgctagtatcagttaatgattt
aaaatctttaccaattgcttatactttgaaatcaccaatgggaacagaag
ttagtcaagatgctaaaaacgctattatggacaacgtcacattcttaaga
aaacaaggattcaaagtaacagagatagacttaccaattgatggtagagc
attaatgcgtgattattcaaccttggctattggcatgggaggagcttttt
caacaattgaaaaagacttaaaaaaacatggttttactaaagaagacgtt
gatcctattacttgggcagttcatgttatttatcaaaattcagataaggc
tgaacttaagaaatctattatggaagcccaaaaacatatggatgattatc
gtaaggcaatggagaagcttcacaagcaatttcctattttcttatcgcca
acgaccgcaagtttagcccctctaaatacagatccatatgtaacagagga
agataaaagagcgatttataatatggaaaacttgagccaagaagaaagaa
ttgctctctttaatcgccagtgggagcctatgttgcgtagaacaccttttt
acacaaattgctaatatgacaggactcccagctatcagtatcccgactta
cttatctgagtctggtttacccatagggacgatgttaatggcaggtgcaa
actatgatatggtattaattaaatttgcaactttctttgaaaaacatcat
ggttttaatgttaaatggcaaagaataatagataaagaagtgaaaccatc
tactggcctaatacagcctactaactccctctttaaagctcattcatcat
tagtaaatttagaagaaaattcacaagttactcaagtatctatctctaaa
aaatggatgaaatcgtctgttaaaaataaaccatccgtaatggcatatca
aaaagca

SEQ ID NO: 4802
STRAIN 090
AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAA
ATACTATCGTTCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCA
GAATCAGGACAATCTGTAATAGGTCAAGTAAAACCAGATAATTCTGCGGC
GCTTACAACAGTTGACACGCCTCATCATATTTCAGCTCCAGATGCTTTAA
AAACAACTCAATCAAGTCCTGTCGTTGAGAGTACTTCTACTAAGTTAACT
GAAGAGACTTACAAACAAAAAGATGGTAAAGATTTAGCCAACATGGTGAG
AAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATACGATATTA
TTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAA
GAAGCTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTTTT
AGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTG
AAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGAC
AGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACA
AACGAACTTTCCAGAGTATGGGTGGCGTAATATAACAGATTCTAAATTAT
ACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCT
TCTGGTGGAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAG
CGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCT
TGGTAGGTTTAAAACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGAT
TCGTATAGTACAGCAGTTCATTTTCCATTAACTAAGTCATCTAGAGACGC
AGAAACATTATTAACTTATCTAAAGAAAAGCGATCAAACGCTAGTATCAG
TTAATGATTTAAAATCTTtACCAATTGCTTATACTTTGAAATCACCAATG
GGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCAC
ATTCTTAAGAAAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTG
ATGGTAGAGCATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGA
GGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAAACATGGTTTTACTAA
AGAAGACGTTGATCCTATTACTTGGGCAGTTCATGTTATTTATCAAAATT
CAGATAAGGCTGAACTTAAGAAATCTATTATGGAAGCCCAAAAACATATG
GATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCCTATTTT
CTTATCGCCAACGACCGCAAGTTTAGCCCCTCTAAATACAGATCCATATG
TAACAGAGGAAGATAAAAGAGCGATTTATAATATGGAAAACTTGAGCCAA
GAAGAAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG
AACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGCTATCAGTA
TCCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATG
GCAGGTGCAAACTATGATATGGTATTAATTAAATTTGCAACTTTCTTTGA
AAAACATCATGGTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAG
TGAAACCATCTACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCT
CATTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC
TATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAA
TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

STRAIN A909
TACTACAAATACTATCGTTCAAACTAATGACAGTAATCCTACCGCAAAAT
TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAAACCAGATAAT
TCTGCGGCGCTTACAACAGTTGACACGCCTCATCATATTTCAGCTCCAGA
TGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGAGTACTTCTACTA
AGTTAACTGAAGAGACTTACAAACAAAAAGATGGTCAAGATTTAGCCAAC
ATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATA
CGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA
GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAG
CCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCACAGTATTAA
AGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCA
CATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATT
TTAGGACAAACGAACTTTCCAGAGTATGGGTGGCGTAATATAACAGATTC
TAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG
GTGGCTCTTCTGGTGGAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCA
ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTG
GACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTGAGTAATGAAA
AGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTAAcTAAGTCATCT
AGAGACGCAGAAACATTATTAACTTATCTAAAGAAAAGCGATCAAACGCT
AGTATCAGTTAATGATTTAAAATCTTTACCAATTGCTTATACTTTGAAAT
CACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGAC
AACGTCACaTTCTTAAGAAAACAAGGATTCAAAGTAACAGAGATAGACTT
ACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTTGGCTATTG
GCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAAACATGGT
TTTACTAAAGAAGACGTTGATCCTATTACTTGGGCAGTTCATGTTATTTA
TCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTATGGAAGCCCAAA
AACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTT
CCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCTCTAAATACAGA
TCCATATGTaACAGAGGAAGATAAAAGAGCGATTTATAATATGGAAAACT
TGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATG
TTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGC
TATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGA
TGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAAATTTGCAACT
TTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGAATAATAGA
TAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTAACTCCCTCT
TTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACT
CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACC
ATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4804
STRAIN COH1
AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT
ACTATCGTTCAAACTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA
ATCAGGACAATCTGTAATAGGTCAAGTAAAACCAGCTAATTCTGCGGCGC
TTACAACAGTTGACACGCCTCATATTTCAGCTCCAGATGCTTTAAAAACA
ACTCAATCAAGTCCTGTCGTTGAGAGTCCTTCTACTAAGTTAACTGAAGA
GACATACAAACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTG
GTCAAGTTACTAGTGAGGAACTCGTCAATATGGCATACGATATTATCGCT
AAAGAAAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGC
CATTGAAGAGGCTAGAAAACTTAAAGATACTAATCAGCCGTTTTTAGGTG
TTCCcTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACC
AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG
CTATGTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGA
ATTTTCCAGAGTATGGGTGGCGTAATATAACAGACTCTAAATTATACGGT
CCAACGCATAATCCTTGGAATCTTGCTCATAACGCTGGTGGCTCTTCTGG
TGGAAGTGCAGCAGCTATTGCTAGCGGAATGACGCCAATTGCTAGCGGCA
GTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCTTAGTA
GGTTTAAAACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGATTCGTA
TAGTACAGCAGTTCATTTTCCATTAACTAAGTCATCTAGAGACGCAGAAA
CATTGTTAACTTACCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAAT
GATTTAAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAAC
AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGGACAACGTCACATTCT
TAAGAAAACAAGGATTCAAAGTGACAGAGATAGATTtACCAATTGATGGT
AGAGCATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGC
TTTTTCAACAATTGAAAAAGACTTAAAAAAACATGGTTTTACTAAAGAAG
ACGTTGATCCCATTACTTGGGCAGTTCATGTTATTTATCAAAATTCAGAT
AAGGCTGAACTTAAGAAATCTATTGTGGAAGCCCAAAAACATATGGATGA
TTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCCTATTTTCTTAT
CGCCAACGACCGCAAgTTTAGCCCCTCTAAATACAGATCCATATGTAACA
GAGAAAGATAAAAGAGCGATTTATAATATGGAAAACTTGAGCCAAGAAGA
AAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC
CTTTTACACCAATTGCTAATAtGACAGGACTCCCAGCTATCAGTATCCCG
ACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGG
TGCAAACTATGATATGGTATTAATTAAATTTGCAACTTTCTTTGAAAAAC
ATCATGGTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAA
CCATCTGCTGACCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTC
ATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCT
CTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA
TATCAAAAAGCA

SEQ ID NO: 4805
STRAIN M732
TCAGTAGCTCCTACTACAAATACTATCGTTCAAACTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTTGCATCAGAATCAGGACAATCTGTAATAGGTCAAGTAA
AACCAGCTAATTCTGCGGCGCTTACAACAGTTGACACGCCTCATATTTCA
GCTCCAGATGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGAGTCC
TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGATT
TAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCAAT
ATGGCATACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAGTCAT
TACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAAGATA
CTAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCAC
AGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAA
AATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGAT
TTATTATTTTAGGACAAACGAATTTTCCAGAGTATGGGTGGCGTAATATA
ACAGACTCTAAATTATACGGTCnAACGCATAATCCTTGGGATCTTGCTCA
TAACGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCTATTGCTAGCGGAA
TGACGCCAATTGCTAGCGGCAGTGATGCTGGTGGTTCTATCCGTATTCCA
TCTTCTTGGACGGGCTTAGTAGGTTTAAAACCAACAAGAGGATTGGTGAG
TAATGAAAAGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTAACTA
AGTCATCTAGAGACGCAGAAACATTGTTAACTTACCTAAAGAAAAGCGAT
CAAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTGCTTATAC
TTTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCTA
TTATGGACAACGTCACATTCTTAAGAAAACAAGGATTCAAAGTGACAGAG
ATAGATTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTT
GGCTATTGGCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAA
AACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGTTCAT
GTTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTGTGGA
AGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACA
AGCAATTTCCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCTCTA
AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGATTTATAATAT
GGAAAACTTGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAGTGGG
AGCCTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATATGACAGGA
CTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCAT
AGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAAAT
TTGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGA
ATAATAGATAAAGAAGTGAAACCATCTGCTGACCTAATACAGCCTACTAA
CTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCAC
AAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAA
AATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4806
STRAIN 18RS21
AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAAATACTATCGT
TCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCAGAATCAGGAC
AATCTGTAATAGGTCAAGTAAAACCAGATAATTCTGCGGCGCTTACAACA
GTTGACACGCCTCATCATATTTCAGCTCCAGATGCTTTAAAAACAACTCA
ATCAAGTCCTGTCGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT
ACAAACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTGGTCAA
GTTACTAGTGAGGAACTCGTTAATATGGCATACGATATTATTGCTAAAGA
AAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCTATTG
AAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTTTTAGGTGTTCCC
TTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAA
TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAGCTATG
TCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGAACTTT
CCAGAGTATGGGTGGCGTAATATAACAGATTCTAAATTATACGGTCTAAC
GCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAA
GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAGCGGTAGTGAT
GCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCTTGGTAGGTTT
AAAACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGATTCGTATAGTA
CAGCAGTTCATTTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTA
TTAACTTATCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAATGATTT
AAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAG
TTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCACATTCTTAAGA
AAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGC
ATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTTT
CAACAATTGAAAAAGACTTAAAAAAACATGGTTTTACTAAAGAAGACGTT
GATCCTATTACTTGGGCAGTTCATGTTATTTATCAAAATTCAGATAAGGC
TGAACTTAAGAAATCTATTATGGAAGCCCAAAAACATATGGATGATTATC
GTAAGGCAATGGAGAAGCTTCACAAGCAATTTCCTATTTTCTTATCGCCA
ACGACCGCAAGTTTAGCCCCTCTAAATACAGATCCATATGTAACAGAGGA
AGatAAAAGAGCGATTTATAATATGGAAAACTTGAGCCAAGAAGAAAGAA
TTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTT
ACACAAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCGACTTA
CTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAA
ACTATGATATGGTATTAATTAAATTTGCAACTTTCTTTGAAAAACATCAT
GGTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAACCATC
TACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCAT
TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTCTAAA
AAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCA
AAAAGCA

SEQ ID NO: 4807
STRAIN M781
TGCTTCAGTAGCTCCTACTACAAATACTATCGTTCAAACTAATGACAGTA
ATCCTACCGCAAAATTTGCATCAGAATCAGGACAATCTGTAATAGGTCAA
GTAAAACCAGCTAATTCTGCGGCGCTTACAACAGTTGACACGCCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGA
GTCCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAA
GATTTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGT
CAATATGGCATACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAG
TCATTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAA
GATACTAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGG
GCACAGTATtAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATG
GAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTA
GGATTTATTATTTTAGGACAAACGaATTTTCCAGAGTATGGGTGGCGTAA
TATAACAGACTCTAAATTATACGGTCCAACGCATAATCCTTGGAaTCTTG
CTCATAACGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCTATTGCTAGC
GGAATGACGCCAATTGCTAGCGGCAGTGATGCTGGTGGTTCTATCCGTAT
TCCATCTTCTTGGACGGGCTTAGTAGGTTTAAAACCAACAAGAGGATTGG
TGAGTAATGAAAAGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTA
ACTAAGTCATCTAGAGACGCAGAAACATTGTTAACTTACCTAAAGAAAAG
CGATCAAACGCTAGTATCAGTTAATGATTTAAAaTCTTTACCAATTGCTT
ATACTTTGAAATCACCAATGGGAACAGAAgTTAGTCAAGATGCTAAAAAT
GCTATTATGGACAACGTCACATTCTTAAGAGAACAAGGATTCAAAGTGAC
AGAGATAGATTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAA
CCTTGGCTATTGGCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTA
AAAAAACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGT
TCATGTTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTG
TGGAAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTT
CACAAGCAATTTCCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCC
TCTAAATACAGATCCATATGTAACAGaGaAAGATAAAAGAGCGATTTATA
ATATGGAAAACTTGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAG
TGGGAGCCTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATAtGAC
AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC
CCATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATT
AAATTTGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCA
AAGAATAATAGATAAAGAAGTGAAACCATCTGCTGACCTAATACAGCCTA
CTAACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAAT
TCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGT
TAAAAATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4810
STRAIN CJB110
TAGTTCCTACTACAAATACTATCGTTCAAACTAATGACAGTAATCCTACC
GCAAAATTTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAAACC
AGATAATTCTGCGGCGCTTACAACAGTTGACACGCCTCATCATATTTCAG
CTCCAGATGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGAGTACT
TCTACTAAGTTAACTGAAGAGACTTACAAACAAAAAGATGGTAAAGATTT
AGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATA
TGGCATACGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATT
ACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGATAC
CAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCACA
GTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAAA
ATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGATT
TATTATTTTAGGACAAACGAACTTTCCAGAGTATGGGTGGCGTAATATAA
CAGATTCTAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCAT
AATGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGCCATTGCTAGCGGAAT
GACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCCAT
CTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTGAGT
CATGAAAAGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTAACTAA
GTCATCTAGAGACGCAGAAACATTATTAACTTATCTAAAGAAAAGCGATC
AAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTGCTTATACT
TTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTAT
TATGGACAACGTCACATTCTTAAGAAAACAAGGATTCAAAGTAACAGAGA
TAGACTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTTG
GCTATTGGCATGGGAgGAGCTTTTTCAACaATTGAAAAAGAcTTAaAAAA
AcATGGTTTTACTAAAGAAGACGTTGATCCTATTACTTGGGCAGTTCATG
TTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTATGGAA
GCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAA
GCAATTTCCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCTCTAA
ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTTATAATATG
GAAAACTTGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAGTGGGA
GCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATAtGACAGGAC
TCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA
gGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAAATT
TGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGAA
TAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTAAC
TCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACA
AGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAA
ATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4811
STRAIN 1169NT
AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAATACTATCGT
TCAAACTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAATCAGGAC
AATCTGTAATATGTCAAGTAAAACCAGATAATTCTGCGGCGCTTACAACA
GTTGACACGCCTCATATTTCAGCTCCAGATGATTTAAAAACAACTCAATC
AAGTCCTGTCGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA
AACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAGAAGTGGTCAAGTT

Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA
CCCTTCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG
AGGCTAGAAAACTTAAAGATACTAATCAGCCATTTTTAGGTGTTCCCTTG
TTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAATGG
CTTGATCTATGCAGATGGAAAAATtaGCACATTTGACAGTAGCTATGTCA
AAAAATATAAAGATTTAGGATTTATTATTTTAGGACAAACGAACTTTCCA
GAGTATGGGTGGCGTAATATAACAGATTCTAAATTATACGGTCCAACGCA
TAACCCTCGGAATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAAGTG
CAGCAGCCATTGCTAGCGGrATGACGCCAATTGCTAGCGGTAGTGATGCT
GGTGGTTCTATCCGtATTCCATCTTCTTGGACGGGCTTGGTAGGTTTAAA
ACCAACAAGAGGATTGGTGAGTAATGAAAAGCCAGATTCGTATAGTACAG
CAGTTCATTTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTATTA
ACTTATCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAATGATTTAAA
ATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAGTTA
GTCAAGATGCTAAAAACGCTATTATGGACAACGTCACATTCTTAAGAAAA
CAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGCATT
AATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTTTCAA
CAATTGAAAAAGACTTAAAAAAACATGGTTTTACTAAAGAAGACGTTGAT
CCTATTACTTGGGCAGTTCATGTTATTTATCAAAATTCAGATAAGGCTGA
ACTTAAGAAATCTATTATGGAAGCCCAAAAACATATGGATGATTATCGTA
AGGCAATGGAGAAGCTTCACAAGCAATTTCCTATTTTCTTATCGCCAACG
ACCGCAAGTTTAGCCCCTCTAAATACAGAtCCATATGTAACAGAGGAAGA
TAAAAGAGCGATTTATAATATGGAAAACTTGAGCCAAGAAGAAAGAATTG
CTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTTACA
CAAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCGACTTACTT
ATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAAACT
ATGATATGGTATTAATTAAATTTGCAACTTTCTTTGAAAAACATCATGGT
TTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAACCATCTAC
TGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCATTAG
TAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTCTAAAAAA
TGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCAAAA
AGCA

SEQ ID NO: 4812
STRAIN JM9130013
TTCAGTAGCTCCTACTACAAATACTATCGTTCAAACTAATGACAGTAATC
CTACCGCAAAATTTTCATCAGAATCAGGACAATCTGTAATAGGTCAAGTA
AAACCAGCTAATTCTGTGGCGCTTACAACAGTTGACACGCCTCATATTTC
AGCTCCAGATGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGAGTC
CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGAG
TTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCAA
TATGGCATACGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCA
TTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGAT
ACCAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCA
CAGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGGTGGAA
AAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGA
TTTATTATTTTAGGACAAACGAACTTTCCAGAGTATGGATGGCGCAATAT
AACAGATTCTAAATTATACGGTCCAACGCATAACCCTTGGAATCTTGCTC
ATAATGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGTTATTGCTAGCGGG
ATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCC
ATCTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTGA
GTAATGAAAAGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTAACT
AAGTCATCTAGAGACGCAGAAACATTATTAACTTATCTAAAGAAAAGCGA
TCAAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTGCTTATA
CTTTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCT
ATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAGA
GATAGACTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCT
TGGCTATTGGTATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAA
AAACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGGAGTTCA
TGTTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTATGG
AAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCAC
AAGCAATTTCCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCTCT
AAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTTATAATA
TGGAAAACTTGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAGTGG
GAGCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGG
ACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCA
TAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAAA
TTTGCAACTTTCTTTGAAAAATATCATGGTTTTAATGTTAAATGGCAAAG
AATAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACTA
ACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCA
CAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAA
AAATAAACCATCCGTAATGGCATAT

SEQ ID NO: 4813
STRAIN H36B
CTTCAGTAGTTCCTACTACAAATACTATCGTTCAAACTAATGACAGTAAT
CCTACCGCAAAATTTTCATCAGAATCAGGACAATCTGTAATAGGTCAAGT
AAAACCAGCTAATTCTGTGGCGCTTACAACAGTTGACACGCCTCATATTT
CAGCTCCAGATGCTTTAAAAACAACTCAATCAAGTCCTGTCGTTGAGAGT
CCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGA
TTTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCA
ATATGGCATaCGATAtTATTGCTAAAGAAAACCCATCTTTAAATGCAGTC
ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

```
TACCAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGC
ACAGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGGTGGA
AAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGG
ATTTATTATTTTAGGACAAACGAACTTTCCAGAGTATGGATGGCGCAATA
TAACAGATTCTAAATTATACGGTCCAACGCATAACCCTTGGAATCTTGCT
CATAATGCTGGTGGCTCTTCTGGTGGAAGTGCAGCAGTTATTGCTAGCGG
GATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTC
CATCTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTG
AGTAATGAAAAGCCAGATTCGTATAGTACAGCAGTTCATTTTCCATTAAC
TAAGTCATCTAGAGACGCAGAAACATTATTAACTTATCTAAAGAAAAGCG
ATCAAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTGCTTAT
ACTTTGAAATCACCAATGGGAACAGAAGTTAGTCAAGATGCTAAAAATGC
TATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAG
AGATAGACTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACC
TTGGCTATTGGTATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAA
AAAACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGTTC
ATGTTATTTATCAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTATG
GAAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA
CAAGCAATTTCCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCCTC
TAAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTTATAAT
ATGGAAAACTTGAGCCAAGAAGAAAGAATTGCTCTCTTTAATCGCCAGTG
GGAGCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAG
GACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC
ATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAA
ATTTGCAACTTTCTTTGAAAAATATCATGGTTTTAATGTTAAATGGCAAA
GAATAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCTACT
AACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTC
ACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTA
AAAATAAA
```

```
PRETTY of: /biotmp/msa71927.2{*}   January 22, 2003 07:23  ..

                           1                                                   50
   msa71927.2{173_18RS21}  aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT
     msa71927.2{173_2603}  aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT
     msa71927.2{173_A909}  ---------- ---------- ---------- --TACTACAA ATACTATCGT
      msa71927.2{173_090}  aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT
   msa71927.2{173_CJB110}  ---------- ---------- -----tagtt ccTACTACAA ATACTATCGT
     msa71927.2{173_COH1}  aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT
     msa71927.2{173_M781}  ---------- -------tgc ttcagtagct ccTACTACAA ATACTATCGT
     msa71927.2{173_M732}  ---------- ---------- -tcagtagct ccTACTACAA ATACTATCGT
     msa71927.2{173_H36B}  ---------- ---------c ttcagtagtt ccTACTACAA ATACTATCGT
msa71927.2{173_JM9130013}  ---------- ---------- ttcagtagct ccTACTACAA ATACTATCGT
   msa71927.2{173_1169NT}  aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT
                Consensus  ---------- ---------- ---------- --******** **********

                           51                                                 100
   msa71927.2{173_18RS21}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC
     msa71927.2{173_2603}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC
     msa71927.2{173_A909}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC
      msa71927.2{173_090}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC
   msa71927.2{173_CJB110}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC
     msa71927.2{173_COH1}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC
     msa71927.2{173_M781}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC
     msa71927.2{173_M732}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC
     msa71927.2{173_H36B}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC
msa71927.2{173_JM9130013}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC
   msa71927.2{173_1169NT}  TCAAACTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC
                Consensus  ********** ********** ********** ****__**** **********

                           101                                                150
   msa71927.2{173_18RS21}  AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_2603}  AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_A909}  AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
      msa71927.2{173_090}  AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
   msa71927.2{173_CJB110}  AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_COH1}  AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_M781}  AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_M732}  AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
     msa71927.2{173_H36B}  AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA
msa71927.2{173_JM9130013}  AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA
   msa71927.2{173_1169NT}  AATCTGTAAT AtGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
                Consensus  ********** *_******** *******_** ******_*** **********

                           151                                                200
   msa71927.2{173_18RS21}  GTTGACACGC CtcaTCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
     msa71927.2{173_2603}  GTTGACACGC CtcaTCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
     msa71927.2{173_A909}  GTTGACACGC CtcaTCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
      msa71927.2{173_090}  GTTGACACGC CtcaTCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
   msa71927.2{173_CJB110}  GTTGACACGC CtcaTCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
     msa71927.2{173_COH1}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
     msa71927.2{173_M781}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
     msa71927.2{173_M732}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
```

Table 48: Comparative Sequences relating to SAG1474

```
      msa71927.2{173_H36B}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
 msa71927.2{173_JM9130013}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGcTTTAA AAACAACTCA
    msa71927.2{173_1169NT}  GTTGACACGC C...TCATAT TTCAGCTCCA GATGaTTTAA AAACAACTCA
                 Consensus  ********** *---****** ********** ****-***** **********

                            201                                                250
    msa71927.2{173_18RS21}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACtT
      msa71927.2{173_2603}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACtT
      msa71927.2{173_A909}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACtT
       msa71927.2{173_090}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACtT
    msa71927.2{173_CJB110}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACtT
      msa71927.2{173_COH1}  ATCAAGTCCT GTCGTTGAGA GTcCTTCTAC TAAGTTAACT GAAGAGACaT
      msa71927.2{173_M781}  ATCAAGTCCT GTCGTTGAGA GTcCTTCTAC TAAGTTAACT GAAGAGACaT
      msa71927.2{173_M732}  ATCAAGTCCT GTCGTTGAGA GTcCTTCTAC TAAGTTAACT GAAGAGACaT
      msa71927.2{173_H36B}  ATCAAGTCCT GTCGTTGAGA GTcCTTCTAC TAAGTTAACT GAAGAGACaT
 msa71927.2{173_JM9130013}  ATCAAGTCCT GTCGTTGAGA GTcCTTCTAC TAAGTTAACT GAAGAGACaT
    msa71927.2{173_1169NT}  ATCAAGTCCT GTCGTTGAGA GTaCTTCTAC TAAGTTAACT GAAGAGACaT
                 Consensus  ********** ********** **-******* ********** ********-*

                            251                                                300
    msa71927.2{173_18RS21}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_2603}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_A909}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
       msa71927.2{173_090}  ACAAACAAAA AGATGGTaAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
    msa71927.2{173_CJB110}  ACAAACAAAA AGATGGTaAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_COH1}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_M781}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_M732}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
      msa71927.2{173_H36B}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
 msa71927.2{173_JM9130013}  ACAAACAAAA AGATGGTcAA GAgTTAGCCA ACATGGTGAG AAGTGGTCAA
    msa71927.2{173_1169NT}  ACAAACAAAA AGATGGTcAA GAtTTAGCCA ACATGGTGAG AAGTGGTCAA
                 Consensus  ********** *******-** **-******* ********** **********

                            301                                                350
    msa71927.2{173_18RS21}  GTTACTAGTG AGGAACTCGT tAATATGGCA TACGATATTA TtGCTAAAGA
      msa71927.2{173_2603}  GTTACTAGTG AGGAACTCGT tAATATGGCA TACGATATTA TtGCTAAAGA
      msa71927.2{173_A909}  GTTACTAGTG AGGAACTCGT tAATATGGCA TACGATATTA TtGCTAAAGA
       msa71927.2{173_090}  GTTACTAGTG AGGAACTCGT tAATATGGCA TACGATATTA TtGCTAAAGA
    msa71927.2{173_CJB110}  GTTACTAGTG AGGAACTCGT tAATATGGCA TACGATATTA TtGCTAAAGA
      msa71927.2{173_COH1}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TcGCTAAAGA
      msa71927.2{173_M781}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TcGCTAAAGA
      msa71927.2{173_M732}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TcGCTAAAGA
      msa71927.2{173_H36B}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TtGCTAAAGA
 msa71927.2{173_JM9130013}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TtGCTAAAGA
    msa71927.2{173_1169NT}  GTTACTAGTG AGGAACTCGT cAATATGGCA TACGATATTA TtGCTAAAGA
                 Consensus  ********** ********** -********* ********** *-********

                            351                                                400
    msa71927.2{173_18RS21}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
      msa71927.2{173_2603}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
      msa71927.2{173_A909}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
       msa71927.2{173_090}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
    msa71927.2{173_CJB110}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
      msa71927.2{173_COH1}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCcATTG
      msa71927.2{173_M781}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCcATTG
      msa71927.2{173_M732}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCcATTG
      msa71927.2{173_H36B}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
 msa71927.2{173_JM9130013}  AAACCCaTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCtATTG
    msa71927.2{173_1169NT}  AAACCCtTCT TTAAATGCAG TCATTACTAC TAGACGCCAA GAAGCcATTG
                 Consensus  ******-*** ********** ********** ********** *****-****

                            401                                                450
    msa71927.2{173_18RS21}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_2603}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_A909}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
       msa71927.2{173_090}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
    msa71927.2{173_CJB110}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_COH1}  AAGAGGCTAG AAAACTTAAA GATACtAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_M781}  AAGAGGCTAG AAAACTTAAA GATACtAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_M732}  AAGAGGCTAG AAAACTTAAA GATACtAATC AGCCgTTTTT AGGTGTTCCC
      msa71927.2{173_H36B}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
 msa71927.2{173_JM9130013}  AAGAGGCTAG AAAACTTAAA GATACcAATC AGCCgTTTTT AGGTGTTCCC
    msa71927.2{173_1169NT}  AAGAGGCTAG AAAACTTAAA GATACtAATC AGCCaTTTTT AGGTGTTCCC
                 Consensus  ********** ********** *****-**** ****-***** **********

                            451                                                500
    msa71927.2{173_18RS21}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
      msa71927.2{173_2603}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
      msa71927.2{173_A909}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
       msa71927.2{173_090}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
    msa71927.2{173_CJB110}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
      msa71927.2{173_COH1}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
      msa71927.2{173_M781}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
```

Table 48: Comparative Sequences relating to SAG1474

```
     msa71927.2{173_M732}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
     msa71927.2{173_H36B}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
msa71927.2{173_JM9130013}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
   msa71927.2{173_1169NT}  TTGTTAGTCA AGGGGTTAGG GCACAGTATT AAAGGTGGTG AAACCAATAA
                Consensus  ********** ********** ********** ********** **********

                           501                                                550
   msa71927.2{173_18RS21}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_2603}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_A909}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
      msa71927.2{173_090}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
   msa71927.2{173_CJB110}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_COH1}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_M781}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_M732}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
     msa71927.2{173_H36B}  TGGCTTGATC TATGCAGgTG GAAAAATTAG CACATTTGAC AGTAGCTATG
msa71927.2{173_JM9130013}  TGGCTTGATC TATGCAGgTG GAAAAATTAG CACATTTGAC AGTAGCTATG
   msa71927.2{173_1169NT}  TGGCTTGATC TATGCAGaTG GAAAAATTAG CACATTTGAC AGTAGCTATG
                Consensus  ********** *******-** ********** ********** **********

                           551                                                600
   msa71927.2{173_18RS21}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
     msa71927.2{173_2603}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
     msa71927.2{173_A909}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
      msa71927.2{173_090}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
   msa71927.2{173_CJB110}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
     msa71927.2{173_COH1}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAtTTT
     msa71927.2{173_M781}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAtTTT
     msa71927.2{173_M732}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAtTTT
     msa71927.2{173_H36B}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
msa71927.2{173_JM9130013}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
   msa71927.2{173_1169NT}  TCAAAAAATA TAAAGATTTA GGATTTATTA TTTTAGGACA AACGAAcTTT
                Consensus  ********** ********** ********** ********** ******-***

                           601                                                650
   msa71927.2{173_18RS21}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCtAAC
     msa71927.2{173_2603}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCtAAC
     msa71927.2{173_A909}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCtAAC
      msa71927.2{173_090}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCtAAC
   msa71927.2{173_CJB110}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCtAAC
     msa71927.2{173_COH1}  CCAGAGTATG GgTGGCGtAA TATAACAGAc TCTAAATTAT ACGGTCcAAC
     msa71927.2{173_M781}  CCAGAGTATG GgTGGCGtAA TATAACAGAc TCTAAATTAT ACGGTCcAAC
     msa71927.2{173_M732}  CCAGAGTATG GgTGGCGtAA TATAACAGAc TCTAAATTAT ACGGTCnAAC
     msa71927.2{173_H36B}  CCAGAGTATG GaTGGCGcAA TATAACAGAt TCTAAATTAT ACGGTCcAAC
msa71927.2{173_JM9130013}  CCAGAGTATG GaTGGCGcAA TATAACAGAt TCTAAATTAT ACGGTCcAAC
   msa71927.2{173_1169NT}  CCAGAGTATG GgTGGCGtAA TATAACAGAt TCTAAATTAT ACGGTCcAAC
                Consensus  ********** *-*****-** *********- ********** ******-***

                           651                                                700
   msa71927.2{173_18RS21}  GCATAAtCCT tGGgATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_2603}  GCATAAtCCT tGGgATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_A909}  GCATAAtCCT tGGgATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
      msa71927.2{173_090}  GCATAAtCCT tGGgATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
   msa71927.2{173_CJB110}  GCATAAtCCT tGGgATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_COH1}  GCATAAtCCT tGGaATCTTG CTCATAAcGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_M781}  GCATAAtCCT tGGaATCTTG CTCATAAcGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_M732}  GCATAAtCCT tGGgATCTTG CTCATAAcGC TGGTGGCTCT TCTGGTGGAA
     msa71927.2{173_H36B}  GCATAAcCCT tGGaATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
msa71927.2{173_JM9130013}  GCATAAcCCT tGGaATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
   msa71927.2{173_1169NT}  GCATAAcCCT cGGaATCTTG CTCATAAtGC TGGTGGCTCT TCTGGTGGAA
                Consensus  ******-*** -**-****** *******-** ********** **********

                           701                                                750
   msa71927.2{173_18RS21}  GTGCAGCAGc cATTGCTAGC GGaATGACGC CAATTGCTAG CGGtAGTGAT
     msa71927.2{173_2603}  GTGCAGCAGc cATTGCTAGC GGaATGACGC CAATTGCTAG CGGtAGTGAT
     msa71927.2{173_A909}  GTGCAGCAGc cATTGCTAGC GGaATGACGC CAATTGCTAG CGGtAGTGAT
      msa71927.2{173_090}  GTGCAGCAGc cATTGCTAGC GGaATGACGC CAATTGCTAG CGGtAGTGAT
   msa71927.2{173_CJB110}  GTGCAGCAGc cATTGCTAGC GGaATGACGC CAATTGCTAG CGGtAGTGAT
     msa71927.2{173_COH1}  GTGCAGCAGc tATTGCTAGC GGaATGACGC CAATTGCTAG CGGcAGTGAT
     msa71927.2{173_M781}  GTGCAGCAGc tATTGCTAGC GGaATGACGC CAATTGCTAG CGGcAGTGAT
     msa71927.2{173_M732}  GTGCAGCAGc tATTGCTAGC GGaATGACGC CAATTGCTAG CGGcAGTGAT
     msa71927.2{173_H36B}  GTGCAGCAGt tATTGCTAGC GGgATGACGC CAATTGCTAG CGGtAGTGAT
msa71927.2{173_JM9130013}  GTGCAGCAGt tATTGCTAGC GGgATGACGC CAATTGCTAG CGGtAGTGAT
   msa71927.2{173_1169NT}  GTGCAGCAGc cATTGCTAGC GGrATGACGC CAATTGCTAG CGGtAGTGAT
                Consensus  *********- -********* **-******* ********** ***-******

                           751                                                800
   msa71927.2{173_18RS21}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
     msa71927.2{173_2603}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
     msa71927.2{173_A909}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
      msa71927.2{173_090}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
   msa71927.2{173_CJB110}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
     msa71927.2{173_COH1}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TaGTAGGTTT
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Table 48: Comparative Sequences relating to SAG1474

```
       msa71927.2{173_M781}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TaGTAGGTTT
       msa71927.2{173_M732}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TaGTAGGTTT
       msa71927.2{173_H36B}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
  msa71927.2{173_JM9130013}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
     msa71927.2{173_1169NT}  GCTGGTGGTT CTATCCGTAT TCCATCTTCT TGGACGGGCT TgGTAGGTTT
                  Consensus  ********** ********** ********** ********** *_********

                             801                                               850
     msa71927.2{173_18RS21}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_2603}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_A909}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
        msa71927.2{173_090}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
     msa71927.2{173_CJB110}  AAAACCAACA AGAGGATTGG TGAGTcATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_COH1}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_M781}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_M732}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
       msa71927.2{173_H36B}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
  msa71927.2{173_JM9130013}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
     msa71927.2{173_1169NT}  AAAACCAACA AGAGGATTGG TGAGTaATGA AAAGCCAGAT TCGTATAGTA
                  Consensus  ********** ********** *****_**** ********** **********

                             851                                               900
     msa71927.2{173_18RS21}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
       msa71927.2{173_2603}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
       msa71927.2{173_A909}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
        msa71927.2{173_090}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
     msa71927.2{173_CJB110}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
       msa71927.2{173_COH1}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTg
       msa71927.2{173_M781}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTg
       msa71927.2{173_M732}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTg
       msa71927.2{173_H36B}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
  msa71927.2{173_JM9130013}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
     msa71927.2{173_1169NT}  CAGCAGTTCA TTTTCCATTA ACTAAGTCAT CTAGAGACGC AGAAACATTa
                  Consensus  ********** ********** ********** ********** *********_

                             901                                               950
     msa71927.2{173_18RS21}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_2603}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_A909}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
        msa71927.2{173_090}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
     msa71927.2{173_CJB110}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_COH1}  TTAACTTAcC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_M781}  TTAACTTAcC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_M732}  TTAACTTAcC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
       msa71927.2{173_H36B}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
  msa71927.2{173_JM9130013}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
     msa71927.2{173_1169NT}  TTAACTTAtC TAAAGAAAAG CGATCAAACG CTAGTATCAG TTAATGATTT
                  Consensus  ********_* ********** ********** ********** **********

                             951                                              1000
     msa71927.2{173_18RS21}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_2603}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_A909}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
        msa71927.2{173_090}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
     msa71927.2{173_CJB110}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_COH1}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_M781}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_M732}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
       msa71927.2{173_H36B}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
  msa71927.2{173_JM9130013}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
     msa71927.2{173_1169NT}  AAAATCTTTA CCAATTGCTT ATACTTTGAA ATCACCAATG GGAACAGAAG
                  Consensus  ********** ********** ********** ********** **********

                             1001                                             1050
     msa71927.2{173_18RS21}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_2603}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_A909}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
        msa71927.2{173_090}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
     msa71927.2{173_CJB110}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_COH1}  TTAGTCAAGA TGCTAAAAAt GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_M781}  TTAGTCAAGA TGCTAAAAAt GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_M732}  TTAGTCAAGA TGCTAAAAAt GCTATTATGG ACAACGTCAc ATTCTTAAGA
       msa71927.2{173_H36B}  TTAGTCAAGA TGCTAAAAAt GCTATTATGG ACAACGTCAt ATTCTTAAGA
  msa71927.2{173_JM9130013}  TTAGTCAAGA TGCTAAAAAt GCTATTATGG ACAACGTCAt ATTCTTAAGA
     msa71927.2{173_1169NT}  TTAGTCAAGA TGCTAAAAAc GCTATTATGG ACAACGTCAc ATTCTTAAGA
                  Consensus  ********** *********_ ********** *********_ **********

                             1051                                             1100
     msa71927.2{173_18RS21}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
       msa71927.2{173_2603}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
       msa71927.2{173_A909}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
        msa71927.2{173_090}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
     msa71927.2{173_CJB110}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
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Table 48: Comparative Sequences relating to SAG1474

```
       msa71927.2{173_COH1}  aAACAAGGAT TCAAAGTgAC AGAGATAGAt TTACCAATTG ATGGTAGAGC
       msa71927.2{173_M781}  gAACAAGGAT TCAAAGTgAC AGAGATAGAt TTACCAATTG ATGGTAGAGC
       msa71927.2{173_M732}  aAACAAGGAT TCAAAGTgAC AGAGATAGAt TTACCAATTG ATGGTAGAGC
       msa71927.2{173_H36B}  aAACAAGGAT TCAAAGTgAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
   msa71927.2{173_JM9130013}  aAACAAGGAT TCAAAGTgAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
     msa71927.2{173_1169NT}  aAACAAGGAT TCAAAGTaAC AGAGATAGAc TTACCAATTG ATGGTAGAGC
                  Consensus  -********* *******-** *********- ********** **********

                             1101                                              1150
     msa71927.2{173_18RS21}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_2603}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_A909}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
        msa71927.2{173_090}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
     msa71927.2{173_CJB110}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_COH1}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_M781}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_M732}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
       msa71927.2{173_H36B}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGtATGGGA GGAGCTTTTT
  msa71927.2{173_JM9130013}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGtATGGGA GGAGCTTTTT
     msa71927.2{173_1169NT}  ATTAATGCGT GATTATTCAA CCTTGGCTAT TGGcATGGGA GGAGCTTTTT
                  Consensus  ********** ********** ********** ***-****** **********

                             1151                                              1200
     msa71927.2{173_18RS21}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_2603}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_A909}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
        msa71927.2{173_090}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
     msa71927.2{173_CJB110}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_COH1}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_M781}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_M732}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
       msa71927.2{173_H36B}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
  msa71927.2{173_JM9130013}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
     msa71927.2{173_1169NT}  CAACAATTGA AAAAGACTTA AAAAAACATG GTTTTACTAA AGAAGACGTT
                  Consensus  ********** ********** ********** ********** **********

                             1201                                              1250
     msa71927.2{173_18RS21}  GATCCtATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_2603}  GATCCtATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_A909}  GATCCtATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
        msa71927.2{173_090}  GATCCtATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
     msa71927.2{173_CJB110}  GATCCtATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_COH1}  GATCCcATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_M781}  GATCCcATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_M732}  GATCCcATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
       msa71927.2{173_H36B}  GATCCcATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
  msa71927.2{173_JM9130013}  GATCCcATTA CTTGGGgAGT TCATGTTATT TATCAAAATT CAGATAAGGC
     msa71927.2{173_1169NT}  GATCCcATTA CTTGGGcAGT TCATGTTATT TATCAAAATT CAGATAAGGC
                  Consensus  *****-**** ******-*** ********** ********** **********

                             1251                                              1300
     msa71927.2{173_18RS21}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_2603}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_A909}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
        msa71927.2{173_090}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
     msa71927.2{173_CJB110}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_COH1}  TGAACTTAAG AAATCTATTg TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_M781}  TGAACTTAAG AAATCTATTg TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_M732}  TGAACTTAAG AAATCTATTg TGGAAGCCCA AAAACATATG GATGATTATC
       msa71927.2{173_H36B}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
  msa71927.2{173_JM9130013}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
     msa71927.2{173_1169NT}  TGAACTTAAG AAATCTATTa TGGAAGCCCA AAAACATATG GATGATTATC
                  Consensus  ********** *********- ********** ********** **********

                             1301                                              1350
     msa71927.2{173_18RS21}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_2603}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_A909}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
        msa71927.2{173_090}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
     msa71927.2{173_CJB110}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_COH1}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_M781}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_M732}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
       msa71927.2{173_H36B}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
  msa71927.2{173_JM9130013}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
     msa71927.2{173_1169NT}  GTAAGGCAAT GGAGAAGCTT CACAAGCAAT TTCCTATTTT CTTATCGCCA
                  Consensus  ********** ********** ********** ********** **********

                             1351                                              1400
     msa71927.2{173_18RS21}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
       msa71927.2{173_2603}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
       msa71927.2{173_A909}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
        msa71927.2{173_090}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
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Table 48: Comparative Sequences relating to SAG1474

```
    msa71927.2{173_CJB110}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
      msa71927.2{173_COH1}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGaA
      msa71927.2{173_M781}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGaA
      msa71927.2{173_M732}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TtACAGAGaA
      msa71927.2{173_H36B}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
 msa71927.2{173_JM9130013}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
   msa71927.2{173_1169NT}  ACGACCGCAA GTTTAGCCCC TCTAAATACA GATCCATATG TaACAGAGgA
                 Consensus  ********** ********** ********** ********** *-******-*

                            1401                                           1450
    msa71927.2{173_18RS21}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_2603}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_A909}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
       msa71927.2{173_090}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
    msa71927.2{173_CJB110}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_COH1}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_M781}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_M732}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
      msa71927.2{173_H36B}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
 msa71927.2{173_JM9130013}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
    msa71927.2{173_1169NT}  AGATAAAAGA GCGATTTATA ATATGGAAAA CTTGAGCCAA GAAGAAAGAA
                 Consensus  ********** ********** ********** ********** **********

                            1451                                           1500
    msa71927.2{173_18RS21}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_2603}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_A909}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
       msa71927.2{173_090}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
    msa71927.2{173_CJB110}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_COH1}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_M781}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_M732}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
      msa71927.2{173_H36B}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
 msa71927.2{173_JM9130013}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
    msa71927.2{173_1169NT}  TTGCTCTCTT TAATCGCCAG TGGGAGCCTA TGTTGCGTAG AACACCTTTT
                 Consensus  ********** ********** ********** ********** **********

                            1501                                           1550
    msa71927.2{173_18RS21}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_2603}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_A909}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
       msa71927.2{173_090}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
    msa71927.2{173_CJB110}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_COH1}  ACACcAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_M781}  ACACcAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_M732}  ACACcAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
      msa71927.2{173_H36B}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
 msa71927.2{173_JM9130013}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
    msa71927.2{173_1169NT}  ACACaAATTG CTAATATGAC AGGACTCCCA GCTATCAGTA TCCCGACTTA
                 Consensus  ****-***** ********** ********** ********** **********

                            1551                                           1600
    msa71927.2{173_18RS21}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_2603}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_A909}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
       msa71927.2{173_090}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
    msa71927.2{173_CJB110}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_COH1}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_M781}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_M732}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
      msa71927.2{173_H36B}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
 msa71927.2{173_JM9130013}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
    msa71927.2{173_1169NT}  CTTATCTGAG TCTGGTTTAC CCATAGGGAC GATGTTAATG GCAGGTGCAA
                 Consensus  ********** ********** ********** ********** **********

                            1601                                           1650
    msa71927.2{173_18RS21}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_2603}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_A909}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
       msa71927.2{173_090}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
    msa71927.2{173_CJB110}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_COH1}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_M781}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_M732}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
      msa71927.2{173_H36B}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAtATCAT
 msa71927.2{173_JM9130013}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAtATCAT
    msa71927.2{173_1169NT}  ACTATGATAT GGTATTAATT AAATTTGCAA CTTTCTTTGA AAAAcATCAT
                 Consensus  ********** ********** ********** ********** ****-*****

                            1651                                           1700
    msa71927.2{173_18RS21}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
      msa71927.2{173_2603}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
      msa71927.2{173_A909}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
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Table 48: Comparative Sequences relating to SAG1474

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      msa71927.2{173_090}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
   msa71927.2{173_CJB110}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
     msa71927.2{173_COH1}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
     msa71927.2{173_M781}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
     msa71927.2{173_M732}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
     msa71927.2{173_H36B}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
msa71927.2{173_JM9130013}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
  msa71927.2{173_1169NT}  GGTTTTAATG TTAAATGGCA AAGAATAATA GATAAAGAAG TGAAACCATC
                Consensus  ********** ********** ********** ********** **********

                           1701                                               1750
   msa71927.2{173_18RS21}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_2603}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_A909}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
      msa71927.2{173_090}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
   msa71927.2{173_CJB110}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_COH1}  TgCTGaCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_M781}  TgCTGaCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_M732}  TgCTGaCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
     msa71927.2{173_H36B}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
msa71927.2{173_JM9130013}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
  msa71927.2{173_1169NT}  TaCTGgCCTA ATACAGCCTA CTAACTCCCT CTTTAAAGCT CATTCATCAT
                Consensus  *-***-**** ********** ********** ********** **********

                           1751                                               1800
   msa71927.2{173_18RS21}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_2603}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_A909}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
      msa71927.2{173_090}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
   msa71927.2{173_CJB110}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_COH1}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_M781}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_M732}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
     msa71927.2{173_H36B}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
msa71927.2{173_JM9130013}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
  msa71927.2{173_1169NT}  TAGTAAATTT AGAAGAAAAT TCACAAGTTA CTCAAGTATC TATCTCTAAA
                Consensus  ********** ********** ********** ********** **********

                           1801                                               1850
   msa71927.2{173_18RS21}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_2603}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_A909}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
      msa71927.2{173'090}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
   msa71927.2{173_CJB110}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_COH1}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_M781}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_M732}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
     msa71927.2{173_H36B}  AAATGGATGA AATCGTCTGT TAAAAATAAA ~~~~~~~~~~ ~~~~~~~~~~
msa71927.2{173_JM9130013}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatat~~
  msa71927.2{173_1169NT}  AAATGGATGA AATCGTCTGT TAAAAATAAA ccatccgtaa tggcatatca
                Consensus  ********** ********** ********** ---------- ----------

                           1851
   msa71927.2{173_18RS21}  aaaagca
     msa71927.2{173_2603}  aaaagca
     msa71927.2{173_A909}  aaaagca
      msa71927.2{173_090}  aaaagca
   msa71927.2{173_CJB110}  aaaagca
     msa71927.2{173_COH1}  aaaagca
     msa71927.2{173_M781}  aaaagca
     msa71927.2{173_M732}  aaaagca
     msa71927.2{173_H36B}  ~~~~~~~
msa71927.2{173_JM9130013}  ~~~~~~~
  msa71927.2{173_1169NT}  aaaagca
                Consensus  -------
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SEQ ID NO: 4814
STRAIN 2603 frame: 1
NSTETSASVVPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAP
DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPS
LNAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFD
SSYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIAS
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETL
LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEID
LPIDGRALMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
KSIMEAQKHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATFFEKHHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK
KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4815
STRAIN _090 frame: 1
NSTETSASVVPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAP

Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTEETYKQKDGKDLANMVRSGQVTSEELVNMAYDIIAKENPS
LNAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFD
SSYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIAS
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETL
LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEID
LPIDGRALMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
KSIMEAQKHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATFFEKHHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK
KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4816
STRAIN A909 frame: 2
TTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSSPV
VESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTRRQE
AIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSYVKKYKDLG
FIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIASGMTPIASGSDA
GGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLLTYLKKSDQTL
VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEIDLPIDGRALMRD
YSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHMD
DYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFNRQW
EPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKHHG
FNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSVKNKP
SVMAYQKA

SEQ ID NO: 4817
STRAIN COH1 frame: 1
NSTETSASVAPTTNTIVQTNDSNPTAKFASESGQSVIGQVKPANSAALTTVDTPHISAPD
ALKTTQSSPVVESPSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSL
NAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDS
SYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWNLAHNAGGSSGGSAAAIASG
MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLL
TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEIDL
PIDGRALMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKK
SIVEAQKHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEKDKRAIYNMENLSQE
ERIALFNRQWEPMLRRTPFTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
FATFFEKHHGFNVKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKK
WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4818
STRAIN M732 frame: 1
SVAPTTNTIVQTNDSNPTAKFASESGQSVIGQVKPANSAALTTVDTPHISAPDALKTTQS
SPVVESPSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTR
RQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSYVKKYK
DLGFIILGQTNFPEYGWRNITDSKLYGXTHNPWDLAHNAGGSSGGSAAAIASGMTPIASG
SDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLLTYLKKSD
QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEIDLPIDGRAL
MRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQK
HMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEKDKRAIYNMENLSQEERIALFN
RQWEPMLRRTPFTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEK
HHGFNVKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSVK
NKPSVMAYQKA

SEQ ID NO: 4819
STRAIN 18RS21 frame: 1
NSTETSASVVPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAP
DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPS
LNAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFD
SSYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIAS
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETL
LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEID
LPIDGRALMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELK
KSIMEAQKHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATFFEKHHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK
KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4820
STRAIN M781 frame: 2
ASVAPTTNTIVQTNDSNPTAKFASESGQSVIGQVKPANSAALTTVDTPHISAPDALKTTQ
SSPVVESPSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITT
RRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSYVKKY
KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWNLAHNAGGSSGGSAAAIASGMTPIAS
GSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLLTYLKKS
DQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLREQGFKVTEIDLPIDGRA
LMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
KHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEKDKRAIYNMENLSQEERIALF
NRQWEPMLRRTPFTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFE
KHHGFNVKWQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSV
KNKPSVMAYQKA

SEQ ID NO: 4821
STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSS
PVVESTSTKLTEETYKQKDGKDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTRR
QEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSYVKKYKD
LGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSAAAIASGMTPIASGS
DAGGSIRIPSSWTGLVGLKPTRGLVSHEKPDSYSTAVHFPLTKSSRDAETLLTYLKKSDQ
TLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEIDLPIDGRALM
RDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKH
MDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFNR
QWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKH
HGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSVKN
KPSVMAYQKA

SEQ ID NO: 4822
STRAIN 1169NT frame: 1
NSTETSASVAPTTNTIVQTNDSNPTAKFASESGQSVICQVKPDNSAALTTVDTPHISAPD
DLKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSL
NAVITTRRQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYADGKISTFDS
SYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPRNLAHNAGGSSGGSAAAIASG
MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLL
TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFLRKQGFKVTEIDL
PIDGRALMRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKK
SIMEAQKHMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQE
ERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
FATFFEKHHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKK
WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4823
STRAIN JM9130013 frame: 2
SVAPTTNTIVQTNDSNPTAKFSSESGQSVIGQVKPANSVALTTVDTPHISAPDALKTTQS
SPVVESPSTKLTEETYKQKDGQELANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTR
RQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYAGGKISTFDSSYVKKYK
DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWNLAHNAGGSSGGSAAVIASGMTPIASG
SDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLLTYLKKSD
QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVIFLRKQGFKVTEIDLPIDGRAL
MRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWGVHVIYQNSDKAELKKSIMEAQK
HMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN
RQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEK
YHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSVK
NKPSVMAY

SEQ ID NO: 4824
STRAIN H36B frame: 3
SVVPTTNTIVQTNDSNPTAKFSSESGQSVIGQVKPANSVALTTVDTPHISAPDALKTTQS
SPVVESPSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAYDIIAKENPSLNAVITTR
RQEAIEEARKLKDTNQPFLGVPLLVKGLGHSIKGGETNNGLIYAGGKISTFDSSYVKKYK
DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWNLAHNAGGSSGGSAAVIASGMTPIASG
SDAGGSIRIPSSWTGLVGLKPTRGLVSNEKPDSYSTAVHFPLTKSSRDAETLLTYLKKSD
QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVIFLRKQGFKVTEIDLPIDGRAL
MRDYSTLAIGMGGAFSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQK
HMDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN
RQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEK
YHGFNVKWQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKWMKSSVK
NK

```
PRETTY of: /biotmp/msa72034.2{*}   January 22, 2003 07:25  ..

                               1                                                   50
       msa72034.2{173_090}   nstetsasvv pTTNTIVQTN DSNPTAKFvS ESGQSVIgQV KPdNSaALTT
     msa72034.2{173_18RS21}   nstetsasvv pTTNTIVQTN DSNPTAKFvS ESGQSVIgQV KPdNSaALTT
      msa72034.2{173_2603}   nstetsasvv pTTNTIVQTN DSNPTAKFvS ESGQSVIgQV KPdNSaALTT
      msa72034.2{173_A909}   ~~~~~~~~~~ ~TTNTIVQTN DSNPTAKFvS ESGQSVIgQV KPdNSaALTT
    msa72034.2{173_CJB110}   ~~~~~~~~~v pTTNTIVQTN DSNPTAKFvS ESGQSVIgQV KPdNSaALTT
      msa72034.2{173_COH1}   nstetsasva pTTNTIVQTN DSNPTAKFaS ESGQSVIgQV KPaNSaALTT
      msa72034.2{173_M732}   ~~~~~~~sva pTTNTIVQTN DSNPTAKFaS ESGQSVIgQV KPaNSaALTT
      msa72034.2{173_M781}   ~~~~~~asva pTTNTIVQTN DSNPTAKFaS ESGQSVIgQV KPaNSaALTT
    msa72034.2{173_1169NT}   nstetsasva pTTNTIVQTN DSNPTAKFaS ESGQSVIcQV KPdNSaALTT
      msa72034.2{173_H36B}   ~~~~~~~svv pTTNTIVQTN DSNPTAKFsS ESGQSVIgQV KPaNSvALTT
 msa72034.2{173_JM9130013}   ~~~~~~~sva pTTNTIVQTN DSNPTAKFsS ESGQSVIgQV KPaNSvALTT
                 Consensus   ---------- -********* ********-* *******-** **-**-****

                               51                                                 100
       msa72034.2{173_090}   VDTphHISAP DaLKTTQSSP VVEStSTKLT EETYKQKDGk dLANMVRSGQ
     msa72034.2{173_18RS21}   VDTphHISAP DaLKTTQSSP VVEStSTKLT EETYKQKDGq dLANMVRSGQ
      msa72034.2{173_2603}   VDTphHISAP DaLKTTQSSP VVEStSTKLT EETYKQKDGq dLANMVRSGQ
      msa72034.2{173_A909}   VDTphHISAP DaLKTTQSSP VVEStSTKLT EETYKQKDGq dLANMVRSGQ
    msa72034.2{173_CJB110}   VDTphHISAP DaLKTTQSSP VVEStSTKLT EETYKQKDGk dLANMVRSGQ
      msa72034.2{173_COH1}   VDT.pHISAP DaLKTTQSSP VVESpSTKLT EETYKQKDGq dLANMVRSGQ
      msa72034.2{173_M732}   VDT.pHISAP DaLKTTQSSP VVESpSTKLT EETYKQKDGq dLANMVRSGQ
      msa72034.2{173_M781}   VDT.pHISAP DaLKTTQSSP VVESpSTKLT EETYKQKDGq dLANMVRSGQ
    msa72034.2{173_1169NT}   VDT.pHISAP DdLKTTQSSP VVEStSTKLT EETYKQKDGq dLANMVRSGQ
      msa72034.2{173_H36B}   VDT.pHISAP DaLKTTQSSP VVESpSTKLT EETYKQKDGq dLANMVRSGQ
 msa72034.2{173_JM9130013}   VDT.pHISAP DaLKTTQSSP VVESpSTKLT EETYKQKDGq eLANMVRSGQ
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Table 48: Comparative Sequences relating to SAG1474

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                Consensus  ***--***** *-******** ****-***** *********- -*********

                           101                                                150
      msa72034.2{173_090}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
   msa72034.2{173_18RS21}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_2603}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_A909}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
   msa72034.2{173_CJB110}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_COH1}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_M732}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_M781}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
   msa72034.2{173_1169NT}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
     msa72034.2{173_H36B}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
msa72034.2{173_JM9130013}  VTSEELVNMA YDIIAKENPS LNAVITTRRQ EAIEEARKLK DTNQPFLGVP
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
      msa72034.2{173_090}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
   msa72034.2{173_18RS21}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_2603}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_A909}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
   msa72034.2{173_CJB110}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_COH1}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_M732}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_M781}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
   msa72034.2{173_1169NT}  LLVKGLGHSI KGGETNNGLI YAdGKISTFD SSYVKKYKDL GFIILGQTNF
     msa72034.2{173_H36B}  LLVKGLGHSI KGGETNNGLI YAgGKISTFD SSYVKKYKDL GFIILGQTNF
msa72034.2{173_JM9130013}  LLVKGLGHSI KGGETNNGLI YAgGKISTFD SSYVKKYKDL GFIILGQTNF
                Consensus  ********** ********** **-******* ********** **********

                           201                                                250
      msa72034.2{173_090}  PEYGWRNITD SKLYGlTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
   msa72034.2{173_18RS21}  PEYGWRNITD SKLYGlTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_2603}  PEYGWRNITD SKLYGlTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_A909}  PEYGWRNITD SKLYGlTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
   msa72034.2{173_CJB110}  PEYGWRNITD SKLYGlTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_COH1}  PEYGWRNITD SKLYGpTHNP wnLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_M732}  PEYGWRNITD SKLYGxTHNP wdLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_M781}  PEYGWRNITD SKLYGpTHNP wnLAHNAGGS SGGSAAaIAS GMTPIASGSD
   msa72034.2{173_1169NT}  PEYGWRNITD SKLYGpTHNP rnLAHNAGGS SGGSAAaIAS GMTPIASGSD
     msa72034.2{173_H36B}  PEYGWRNITD SKLYGpTHNP wnLAHNAGGS SGGSAAvIAS GMTPIASGSD
msa72034.2{173_JM9130013}  PEYGWRNITD SKLYGpTHNP wnLAHNAGGS SGGSAAvIAS GMTPIASGSD
                Consensus  ********** *****-**** --******** ******-*** **********

                           251                                                300
      msa72034.2{173_090}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
   msa72034.2{173_18RS21}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_2603}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_A909}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
   msa72034.2{173_CJB110}  AGGSIRIPSS WTGLVGLKPT RGLVShEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_COH1}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_M732}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_M781}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
   msa72034.2{173_1169NT}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
     msa72034.2{173_H36B}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
msa72034.2{173_JM9130013}  AGGSIRIPSS WTGLVGLKPT RGLVSnEKPD SYSTAVHFPL TKSSRDAETL
                Consensus  ********** ********** *****-**** ********** **********

                           301                                                350
      msa72034.2{173_090}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
   msa72034.2{173_18RS21}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_2603}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_A909}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
   msa72034.2{173_CJB110}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_COH1}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_M732}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_M781}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
   msa72034.2{173_1169NT}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNVtFLR
     msa72034.2{173_H36B}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNViFLR
msa72034.2{173_JM9130013}  LTYLKKSDQT LVSVNDLKSL PIAYTLKSPM GTEVSQDAKN AIMDNViFLR
                Consensus  ********** ********** ********** ********** ******-***

                           351                                                400
      msa72034.2{173_090}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
   msa72034.2{173_18RS21}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_2603}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_A909}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
   msa72034.2{173_CJB110}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_COH1}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_M732}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_M781}  eQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
   msa72034.2{173_1169NT}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
     msa72034.2{173_H36B}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
```

Table 48: Comparative Sequences relating to SAG1474

```
msa72034.2{173_JM9130013}  kQGFKVTEID LPIDGRALMR DYSTLAIGMG GAFSTIEKDL KKHGFTKEDV
                Consensus  -********* ********** ********** ********** **********

                           401                                              450
      msa72034.2{173_090}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
   msa72034.2{173_18RS21}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_2603}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_A909}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
   msa72034.2{173_CJB110}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_COH1}  DPITWaVHVI YQNSDKAELK KSIvEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_M732}  DPITWaVHVI YQNSDKAELK KSIvEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_M781}  DPITWaVHVI YQNSDKAELK KSIvEAQKHM DDYRKAMEKL HKQFPIFLSP
   msa72034.2{173_1169NT}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
     msa72034.2{173_H36B}  DPITWaVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
msa72034.2{173_JM9130013}  DPITWgVHVI YQNSDKAELK KSImEAQKHM DDYRKAMEKL HKQFPIFLSP
                Consensus  *****-**** ********** ***-****** ********** **********

                           451                                              500
      msa72034.2{173_090}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
   msa72034.2{173_18RS21}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_2603}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_A909}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
   msa72034.2{173_CJB110}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_COH1}  TTASLAPLNT DPYVTEkDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_M732}  TTASLAPLNT DPYVTEkDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_M781}  TTASLAPLNT DPYVTEkDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
   msa72034.2{173_1169NT}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
     msa72034.2{173_H36B}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
msa72034.2{173_JM9130013}  TTASLAPLNT DPYVTEeDKR AIYNMENLSQ EERIALFNRQ WEPMLRRTPF
                Consensus  ********** ******-*** ********** ********** **********

                           501                                              550
      msa72034.2{173_090}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
   msa72034.2{173_18RS21}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_2603}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_A909}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
   msa72034.2{173_CJB110}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_COH1}  TpIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_M732}  TpIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_M781}  TpIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
   msa72034.2{173_1169NT}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKhH
     msa72034.2{173_H36B}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKyH
msa72034.2{173_JM9130013}  TqIANMTGLP AISIPTYLSE SGLPIGTMLM AGANYDMVLI KFATFFEKyH
                Consensus  *-******** ********** ********** ********** ********-*

                           551                                              600
      msa72034.2{173_090}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
   msa72034.2{173_18RS21}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_2603}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_A909}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
   msa72034.2{173_CJB110}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_COH1}  GFNVKWQRII DKEVKPSadL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_M732}  GFNVKWQRII DKEVKPSadL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_M781}  GFNVKWQRII DKEVKPSadL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
   msa72034.2{173_1169NT}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
     msa72034.2{173_H36B}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
msa72034.2{173_JM9130013}  GFNVKWQRII DKEVKPStgL IQPTNSLFKA HSSLVNLEEN SQVTQVSISK
                Consensus  ********** *******--* ********** ********** **********

                           601               619
      msa72034.2{173_090}  KWMKSSVKNK psvmayqka
   msa72034.2{173_18RS21}  KWMKSSVKNK psvmayqka
     msa72034.2{173_2603}  KWMKSSVKNK psvmayqka
     msa72034.2{173_A909}  KWMKSSVKNK psvmayqka
   msa72034.2{173_CJB110}  KWMKSSVKNK psvmayqka
     msa72034.2{173_COH1}  KWMKSSVKNK psvmayqka
     msa72034.2{173_M732}  KWMKSSVKNK psvmayqka
     msa72034.2{173_M781}  KWMKSSVKNK psvmayqka
   msa72034.2{173_1169NT}  KWMKSSVKNK psvmayqka
     msa72034.2{173_H36B}  KWMKSSVKNK ~~~~~~~~~
msa72034.2{173_JM9130013}  KWMKSSVKNK psvmay~~~
                Consensus  ********** ---------
```

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901
STRAIN 2603
aaacatccgatacttaatgatcaaaaatccttagcaattgttgaacagat
agaatatgattttgataaattcgataattcagaagcttctttttatgcaa
cattagctagawttcgcgttatggatagagaaatcaaaaaatttattaga
gaaaatccaaatagtcaaatcctttcaattggttgtggacttgatacaag
gtttgaaagagtcgataatggacaaattaggtggtataaccttgatttgc
cagaggttatggagataagaaaattatttttttgaagagcatgaaagagtt
actaatatagcaaaatcagccctagatgaaacttggacacgggaggtaaa
tccccaaaatgccccttttctaatcgtgtcagaaggtgttttaatgtttc
taaaagaagatgacgtagagacttttcttcatatcctgacaaattcattt
agccaatttatggcacaatttgatttgtgtcataaggaaatgattaataa
aggaaagcaacatgatacagtaaagtatatggatacagaatttcagtttg
gtatcacagatggtcatgagattgtggatttagaccctaaattaaagcaa
ataaatctgattaactttacagatgagatgagcaaatttgagttaggcac
acttcgctctttacttccaacaattcgtaaatttaataattgtttaggtg
tgtacgaatataaagcatc

SEQ ID NO: 4902
STRAIN 090
TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG
ATAAATTCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGAATT
CGCGTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAATAG
TCAAATCCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCG
ATAATGGACAAATTAGGTGGTATAACCTTGATTTGCCAGAgGTTATGGAG
ATAAGAAAATTATTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAA
ATCAGCCATAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCC
CTTTTCTAATCGTGTCAGAAGGTGTTTTAATGTTTCTAAAAGAAGATGAC
GTAGAGACTTTTCTTCATATCCTGACAAATTCATTTAGCCAATTTATGGC
ACAATTTGATTTGTGTCATAAGGAAATGATTAATAAAGGAAAGCAACATG
ATACAGTAAAGTATATGGATACAGAATTTCAGTTTGGTATCACAGATGGT
CATGAGATTGTGGATTTAGACCCTAAATTAAAGCAAATAAATCTGATTAA
CTTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTAC
TTCCAACAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAA
GCATC

SEQ ID NO: 4903
STRAIN A909
AAACATCCGATACTTAATGA
TCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAAT
TCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGAATTCGCGTT
ATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAATAGTCAAAT
CcTTTCaATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATG
GACAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGA
AAATTaTTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGC
CCTAGATGaAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCTTTTC
TAATCGTGTCAGAAGGTGTTTTAATGTTtCTAAAAGAAGATGACGTAGAG
ACTTTTcTTCATATCCTGACAAATTCATTTAGCCAATTTATGGCACAATT
TGATTTGTGTCATAAGGAAATGATTAATAAAGGAAAGCAACATGATACAG
TAAAGTATATGGATACAGAATTTCAGTTTGGTATCACAGATGGTCATGAG
ATTGTGGATTTAGACCCTAAATTAAAGCAAATAAATCTGATTAACTTTAC
AGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAA
CAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4904
STRAIN H36B
AAACATCCGATACTTAATGATCAAAAATCCTTAGCA
ATTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGC
TTCTTTTTATGCAaCATTAGCTAGAATTCGCGTTATGGATAGAGAAATCA
AAAAATTTATTAGAGAAAATCCAAATAGTCATATCCTTTCAATTGGCTGT
GgACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTA
TAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAG
AGCATGAAAGAGTTACTAATATAGCAAAATCAGCCcTAGATGAAACTTGG
ACACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGG
TGTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCC
TGACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCAgAAG
GAAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATAC
AGAATTTCAGTTGGGTATCACAGATGGTCATGAAATTGTGGATTTAGACC
CTAAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAA
TTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAA
TAATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4905
STRAIN 18RS21
AACATCCGATACTTAATGATCAAAAATCCTTAGCAAT
TGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCTT
CTTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAA
AAATTTATTAGAGAAAATCCAAATAGTCaAATCCTTTCAATTGGTTGTGG
ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA
ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAG
CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGAC
ACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAgAAGGTG
TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAATTTATGGCACaATTTGATTTGTGTCATAaGGA
AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
AATTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCT
AAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATT
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATA
ATTGTTTAGGTGTGTACGAAtATAaaGCATC

SEQ ID NO: 4906
STRAIN M732
AAACATCCGATACTTAATGATCAAAAATCCTTAGCAATTGTTGAACA
GATAGAATATGATTTGGATAAATTCGATAATTCAGAAGCTTCTTTTTATG
CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAAATTTATT
AGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTGGACTTGATAC
AAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATAACCTTGATT
TGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGA
GTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGACACGGGAGGT
AAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGGTGTTTTAATGT
TTCTAAAAgAAGATGACGTAGAGACTTTTCTTCAtATCCTGACAAATTCA
TTTAGCCAATTTATGGCaCAATTTGATTTGTGTCATAAGGAAATGATTAA
TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAATTTCAGT
TTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCTAAATTAAAG
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAgG
CACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATAATTGTTTAG
GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907
STRAIN COH1
AAACATCCGATACTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTTGGATAAATTCGATAATTCAGAAGCT
TCTTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTG
GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT
AACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGA
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGA
CACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGGT
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT
GACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCATAAGG
AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCC
TAAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAAT
AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4908
STRAIN M781
AAACATCCGATACTTAATGATCA
AAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTGGATAAATTCG
ATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGAATTCGCGTTATG
GATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCT
TTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATGGAC
AAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAA
TTATTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGCCCT
AGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAA
TCGTGTCAGAAGGTGTTTTAATGTTTCTAAAAgAAGATGACGTAGAGACT
TTTCTTCATATCCTGACAAATtCATTTAGCCAATTTAtGGCACAATTTGA
TTTGTGTCATAAGGAAATGATTAATAAAGGAAAGCAACATGATACAGTAA
AGTATATGGATACAGAATTTCAGTTTGGTATCACAGATGGTCATGAGATT
GTGGATTTAgACCCTAAATTAAAGCAAATAAATCTGATTAACTTTACAGA
TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAA
TTCGTAAATTTAATAATtGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4909
STRAIN CJB110
AAACATCCGATACTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCT
TCTTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTG
GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT
AACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGA
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCATAGATGAAACTTGGA
CACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGGT
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT
GACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCATAAGG
AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCC
TAAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAAT
AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4910
STRAIN 1169NT
AAACATCCGATACTTAATGATCAAAAATCCTTAGCAAT
TGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

```
CTTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAA
AAATTTATTAGAGAAAATCCAAATAGTCATATCCTTTCTATTGGTTGTGG
ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA
ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAG
CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGAC
ACAGGAGGTAAATCCCCAAAATGCCCCTTTTCTGATCGTGTCAGAAGGTG
TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTcTTCATATCCTG
ACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGtCAGAAGGA
AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
AATTTCAGTTTGGTATCACAGATGGTCATGAAATTGTGGATTTAGACCCT
AAATTAAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATT
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATA
ATTGTTTAGGTGTGTACGAATATAAAGCATC
```

SEQ ID NO: 4911
STRAIN JM9130013

```
AGCAATTGTTGAACAGATAGAATATGATT
TTGATAAATTCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGA
ATTCGCGTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAA
TAGTCATATCCTTTCAATTGGCTGTGGACTTGATACAAGGTTTGAAAGAG
TCGATAATGGACAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATG
GAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGAGTTACTAATATAGC
AAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATG
CCCCTTTTCTAATCGTGTCAGAAGGTGTTTTAATGTTTCTAAAAGAAGAT
GACGTAGAGACTTTTCTTCATATCCTGACAAATTCATTTAGCCAATTTAT
GGCACAATTTGATTTGTGTCAgAAGGAAATGATTAATAAAGGAAAGCAAC
ATGATACAGTAAAGTATATGGATACAGAATTTCAGTTTGGTATCACAGAT
GGTCATGAAATTGTGGATTTAGACCCTAAATTAAAGCAAATAAATCTGAT
TAACTTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTT
TACTTCCAACAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATAT
AAAGCATC
```

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PRETTY of: /biotmp/msa42193.2{*}   January 21, 2003 05:04  ..

                              1                                                  50
      msa42193.2{176_090}   ~~~~~~~~~~ ~~~~taatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
    msa42193.2{176_CJB110}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
    msa42193.2{176_18RS21}   ~AACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_2603}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_A909}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_COH1}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_M732}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_M781}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
      msa42193.2{176_H36B}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
 msa42193.2{176_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~AGCAATTG TTGAACAGAT
   msa42193.2{176_1169NT}   AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATTG TTGAACAGAT
                Consensus   ********** ****------ ---------- --******** **********

                             51                                                 100
      msa42193.2{176_090}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
    msa42193.2{176_CJB110}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
    msa42193.2{176_18RS21}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_2603}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_A909}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_COH1}   AGAATATGAT TTgGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_M732}   AGAATATGAT TTgGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_M781}   AGAATATGAT TTgGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
      msa42193.2{176_H36B}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
 msa42193.2{176_JM9130013}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
   msa42193.2{176_1169NT}   AGAATATGAT TTtGATAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
                Consensus   ********** **-******* ********** ********** **********

                             101                                                150
      msa42193.2{176_090}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
    msa42193.2{176_CJB110}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
    msa42193.2{176_18RS21}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_2603}   CATTAGCTAG AwTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_A909}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_COH1}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_M732}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_M781}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
      msa42193.2{176_H36B}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
 msa42193.2{176_JM9130013}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
   msa42193.2{176_1169NT}   CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
                Consensus   ********** *-******** ********** ********** **********

                             151                                                200
      msa42193.2{176_090}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
    msa42193.2{176_CJB110}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
    msa42193.2{176_18RS21}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
      msa42193.2{176_2603}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
      msa42193.2{176_A909}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
      msa42193.2{176_COH1}   GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
```

Table 49: Comparative Sequences related to SAG1502

```
     msa42193.2{176_M732}  GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
     msa42193.2{176_M781}  GAAAATCCAA ATAGTCAaAT CCTTTCaATT GGtTGTGGAC TTGATACAAG
     msa42193.2{176_H36B}  GAAAATCCAA ATAGTCAtAT CCTTTCaATT GGcTGTGGAC TTGATACAAG
msa42193.2{176_JM9130013}  GAAAATCCAA ATAGTCAtAT CCTTTCaATT GGcTGTGGAC TTGATACAAG
   msa42193.2{176_1169NT}  GAAAATCCAA ATAGTCAtAT CCTTTCtATT GGtTGTGGAC TTGATACAAG
                Consensus  ********** *******_** ******_*** **_******* **********

                           201                                                250
      msa42193.2{176_090}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
   msa42193.2{176_CJB110}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
   msa42193.2{176_18RS21}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_2603}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_A909}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_COH1}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_M732}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_M781}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
     msa42193.2{176_H36B}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
msa42193.2{176_JM9130013}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
   msa42193.2{176_1169NT}  GTTTGAAAGA GTCGATAATG GACAAATTAG GTGGTATAAC CTTGATTTGC
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
      msa42193.2{176_090}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
   msa42193.2{176_CJB110}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
   msa42193.2{176_18RS21}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_2603}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_A909}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_COH1}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_M732}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_M781}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
     msa42193.2{176_H36B}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
msa42193.2{176_JM9130013}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
   msa42193.2{176_1169NT}  CAGAGGTTAT GGAGATAAGA AAATTATTTT TTGAAGAGCA TGAAAGAGTT
                Consensus  ********** ********** ********** ********** **********

                           301                                                350
      msa42193.2{176_090}  ACTAATATAG CAAAATCAGC CaTAGATGAA ACTTGGACAC gGGAGGTAAA
   msa42193.2{176_CJB110}  ACTAATATAG CAAAATCAGC CaTAGATGAA ACTTGGACAC gGGAGGTAAA
   msa42193.2{176_18RS21}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_2603}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_A909}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_COH1}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_M732}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_M781}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
     msa42193.2{176_H36B}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
msa42193.2{176_JM9130013}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC gGGAGGTAAA
   msa42193.2{176_1169NT}  ACTAATATAG CAAAATCAGC CcTAGATGAA ACTTGGACAC aGGAGGTAAA
                Consensus  ********** ********** *_******** ********** _*********

                           351                                                400
      msa42193.2{176_090}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
   msa42193.2{176_CJB110}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
   msa42193.2{176_18RS21}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_2603}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_A909}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_COH1}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_M732}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_M781}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
     msa42193.2{176_H36B}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
msa42193.2{176_JM9130013}  TCCCCAAAAT GCCCCTTTTC TaATCGTGTC AGAAGGTGTT TTAATGTTTC
   msa42193.2{176_1169NT}  TCCCCAAAAT GCCCCTTTTC TgATCGTGTC AGAAGGTGTT TTAATGTTTC
                Consensus  ********** ********** *_******** ********** **********

                           401                                                450
      msa42193.2{176_090}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
   msa42193.2{176_CJB110}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
   msa42193.2{176_18RS21}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_2603}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_A909}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_COH1}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_M732}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_M781}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
     msa42193.2{176_H36B}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
msa42193.2{176_JM9130013}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
   msa42193.2{176_1169NT}  TAAAAGAAGA TGACGTAGAG ACTTTTCTTC ATATCCTGAC AAATTCATTT
                Consensus  ********** ********** ********** ********** **********

                           451                                                500
      msa42193.2{176_090}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
   msa42193.2{176_CJB110}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
   msa42193.2{176_18RS21}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
     msa42193.2{176_2603}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
     msa42193.2{176_A909}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
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Table 49: Comparative Sequences related to SAG1502

```
     msa42193.2{176_COH1}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
     msa42193.2{176_M732}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
     msa42193.2{176_M781}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAtAAGGAAA TGATTAATAA
     msa42193.2{176_H36B}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAgAAGGAAA TGATTAATAA
msa42193.2{176_JM9130013}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAgAAGGAAA TGATTAATAA
   msa42193.2{176_1169NT}  AGCCAATTTA TGGCACAATT TGATTTGTGT CAgAAGGAAA TGATTAATAA
                Consensus  ********** ********** ********** **-******* **********

                           501                                                550
      msa42193.2{176_090}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
   msa42193.2{176_CJB110}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
   msa42193.2{176_18RS21}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_2603}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_A909}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_COH1}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_M732}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_M781}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
     msa42193.2{176_H36B}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTgG
msa42193.2{176_JM9130013}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
   msa42193.2{176_1169NT}  AGGAAAGCAA CATGATACAG TAAAGTATAT GGATACAGAA TTTCAGTTtG
                Consensus  ********** ********** ********** ********** ********-*

                           551                                                600
      msa42193.2{176_090}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
   msa42193.2{176_CJB110}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
   msa42193.2{176_18RS21}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_2603}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_A909}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_COH1}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_M732}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_M781}  GTATCACAGA TGGTCATGAg ATTGTGGATT TAGACCCTAA ATTAAAGCAA
     msa42193.2{176_H36B}  GTATCACAGA TGGTCATGAa ATTGTGGATT TAGACCCTAA ATTAAAGCAA
msa42193.2{176_JM9130013}  GTATCACAGA TGGTCATGAa ATTGTGGATT TAGACCCTAA ATTAAAGCAA
   msa42193.2{176_1169NT}  GTATCACAGA TGGTCATGAa ATTGTGGATT TAGACCCTAA ATTAAAGCAA
                Consensus  ********** *********- ********** ********** **********

                           601                                                650
      msa42193.2{176_090}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
   msa42193.2{176_CJB110}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
   msa42193.2{176_18RS21}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_2603}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_A909}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_COH1}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_M732}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_M781}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
     msa42193.2{176_H36B}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
msa42193.2{176_JM9130013}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
   msa42193.2{176_1169NT}  ATAAATCTGA TTAACTTTAC AGATGAGATG AGCAAATTTG AGTTAGGCAC
                Consensus  ********** ********** ********** ********** **********

                           651                                                700
      msa42193.2{176_090}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
   msa42193.2{176_CJB110}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
   msa42193.2{176_18RS21}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_2603}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_A909}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_COH1}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_M732}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_M781}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
     msa42193.2{176_H36B}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
msa42193.2{176_JM9130013}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
   msa42193.2{176_1169NT}  ACTTCGCTCT TTACTTCCAA CAATTCGTAA ATTTAATAAT TGTTTAGGTG
                Consensus  ********** ********** ********** ********** **********

                           701               719
      msa42193.2{176_090}  TGTACGAATA TAAAGCATC
   msa42193.2{176_CJB110}  TGTACGAATA TAAAGCATC
   msa42193.2{176_18RS21}  TGTACGAATA TAAAGCATC
     msa42193.2{176_2603}  TGTACGAATA TAAAGCATC
     msa42193.2{176_A909}  TGTACGAATA TAAAGCATC
     msa42193.2{176_COH1}  TGTACGAATA TAAAGCATC
     msa42193.2{176_M732}  TGTACGAATA TAAAGCATC
     msa42193.2{176_M781}  TGTACGAATA TAAAGCATC
     msa42193.2{176_H36B}  TGTACGAATA TAAAGCATC
msa42193.2{176_JM9130013}  TGTACGAATA TAAAGCATC
   msa42193.2{176_1169NT}  TGTACGAATA TAAAGCATC
                Consensus  ********** *********
```

SEQ ID NO: 4912
STRAIN 2603 frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARXRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4913
STRAIN 090 frame: 2
NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLD
TRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSAIDETWTREVNPQNAPFLI
VSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTEFQFGI
TDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4914
STRAIN A909 frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4915
STRAIN H36B frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCQKEMINKGKQHDTVKYMDTE
FQLGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4916
STRAIN 18RS21 frame: 3
HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIG
CGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQNA
PFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTEF
QFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4917
STRAIN M732 frame: 1
KHPILNDQKSLAIVEQIEYDLDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4918
STRAIN COH1 frame: 1
KHPILNDQKSLAIVEQIEYDLDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4919
STRAIN M781 frame: 1
KHPILNDQKSLAIVEQIEYDLDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4920
STRAIN CJB110 frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSAIDETWTREVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4921
STRAIN 1169NT frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTQEVNPQN
APFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCQKEMINKGKQHDTVKYMDTE
FQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

SEQ ID NO: 4922
STRAIN JM9130013 frame: 2
AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSIGCGLDTRFERV
DNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQNAPFLIVSEGVL
MFLKEDDVETFLHILTNSFSQFMAQFDLCQKEMINKGKQHDTVKYMDTEFQFGITDGHEI
VDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKA

```
 PRETTY of: /biotmp/msa42204.2{*}   January 21, 2003 05:05  ..

                              1                                                  50
       msa42204.2{176_H36B}   khpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
  msa42204.2{176_JM9130013}   ---------- ~AIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
        msa42204.2{176_090}   -----ndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
     msa42204.2{176_18RS21}   ~hpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
       msa42204.2{176_2603}   khpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARxRV MDREIKKFIR
       msa42204.2{176_A909}   khpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
     msa42204.2{176_CJB110}   khpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
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Table 49: Comparative Sequences related to SAG1502

```
      msa42204.2{176_COH1}  khpilndqks lAIVEQIEYD lDKFDNSEAS FYATLARiRV MDREIKKFIR
      msa42204.2{176_M732}  khpilndqks lAIVEQIEYD lDKFDNSEAS FYATLARiRV MDREIKKFIR
      msa42204.2{176_M781}  khpilndqks lAIVEQIEYD lDKFDNSEAS FYATLARiRV MDREIKKFIR
    msa42204.2{176_1169NT}  khpilndqks lAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR
                 Consensus  ---------- -********* -********* *******-** **********

                            51                                               100
      msa42204.2{176_H36B}  ENPNShILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
 msa42204.2{176_JM9130013}  ENPNShILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
       msa42204.2{176_090}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
    msa42204.2{176_18RS21}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
      msa42204.2{176_2603}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
      msa42204.2{176_A909}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
    msa42204.2{176_CJB110}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
      msa42204.2{176_COH1}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
      msa42204.2{176_M732}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
      msa42204.2{176_M781}  ENPNSqILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
    msa42204.2{176_1169NT}  ENPNShILSI GCGLDTRFER VDNGQIRWYN LDLPEVMEIR KLFFEEHERV
                 Consensus  *****-**** ********** ********** ********** **********

                            101                                              150
      msa42204.2{176_H36B}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
 msa42204.2{176_JM9130013}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
       msa42204.2{176_090}  TNIAKSAiDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
    msa42204.2{176_18RS21}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
      msa42204.2{176_2603}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
      msa42204.2{176_A909}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
    msa42204.2{176_CJB110}  TNIAKSAiDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
      msa42204.2{176_COH1}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
      msa42204.2{176_M732}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
      msa42204.2{176_M781}  TNIAKSAlDE TWTrEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
    msa42204.2{176_1169NT}  TNIAKSAlDE TWTqEVNPQN APFLIVSEGV LMFLKEDDVE TFLHILTNSF
                 Consensus  *******-** ***-****** ********** ********** **********

                            151                                              200
      msa42204.2{176_H36B}  SQFMAQFDLC qKEMINKGKQ HDTVKYMDTE FQlGITDGHE IVDLDPKLKQ
 msa42204.2{176_JM9130013}  SQFMAQFDLC qKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
       msa42204.2{176_090}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
    msa42204.2{176_18RS21}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
      msa42204.2{176_2603}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
      msa42204.2{176_A909}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
    msa42204.2{176_CJB110}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
      msa42204.2{176_COH1}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
      msa42204.2{176_M732}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
      msa42204.2{176_M781}  SQFMAQFDLC hKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
    msa42204.2{176_1169NT}  SQFMAQFDLC qKEMINKGKQ HDTVKYMDTE FQfGITDGHE IVDLDPKLKQ
                 Consensus  ********** -********* ********** **-******* **********

                            201                                  239
      msa42204.2{176_H36B}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
 msa42204.2{176_JM9130013}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
       msa42204.2{176_090}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
    msa42204.2{176_18RS21}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
      msa42204.2{176_2603}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
      msa42204.2{176_A909}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
    msa42204.2{176_CJB110}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
      msa42204.2{176_COH1}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
      msa42204.2{176_M732}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
      msa42204.2{176_M781}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
    msa42204.2{176_1169NT}  INLINFTDEM SKFELGTLRS LLPTIRKFNN CLGVYEYKA
                 Consensus  ********** ********** ********** *********
```

Table 50: Comparative Sequences relating to SAG 1024

SEQ ID NO. 5001
STRAIN 2603
ATGAAAAAACAAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA
GCATGTAAGGATTCAAAAATCCCAGAAAACCGCACAAAGGAAGAGTACCAAGCTGAACAA
AATTTTAAACCGTTTTTTGAGTTTTTAGCACAAAAAGATAAAGATTTGAGCAAAATACAA
AAATACTTACTATTAGTATCGGATTCAGGTGATGCATTAGATTTAGAATATTTCTATAGT
ATTCAAGATTTAAAAAAAAATAAGGATTTAGGGAAGTTTGAAACAAGAAAAAGTCAAATA
GAAAAGCCGGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTGAATATTTTAAA
AATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTGATGACTTTATTATCGGA
GCAATGGATACTAAAGAATTAAAAGAATTAAAAAAATTAAAAGTAAAAAGTTATTTATTA
AAACATCCGGAAACTGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCGAAGCTT
ATTAAAAAA

SEQ ID NO. 5002
STRAIN 090
TAAGGATTCAAAAATCCCAGAAAACCGCACAAAG
GAAGAGTACCAAGCTGAACAAAATTTTAAACTGTTTTTTGAGTTTTTAGC
ACAAAAATATAAAGATTTGAACAAAATACAAAAATACTTACTATTAGTAT
CGGATTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTCAAGAT
TTAAAAAAAAATAAGGATTTAGGGAAGTTTGAAACAAGAAAAAGTCAAAT
AGAAAAGCCGGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTG
AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACA
TTTGATGACTTTATTATCGGAGCAATGGATACTAAAGAATTAAAAAAATT
AAAAGTAAAAAGTTATTTATTAAAACATCCGGAAACTGAGTTGAAAGATA
TAACATATGAATTGCCGACACAGTCGAAGCTTATTAAAAAA

SEQ ID NO. 5003
STRAIN 18RS21
TAAGGATTCAAAAATCCCAGAAAACCGCACAAAGGAAG
AGTACCAAGCTGAACAAAATTTTAAACCGTTTTTTGAGTTTTTAGCACAA
AAAGATAAAGATTTGAGCAAAATACAAAAATACTTACTATTAGTATCGGA
TTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTCAAGATTTAA
AAAAAAATAAGGATTTAGGGAAGTTTGAAACAAGAAAAAGTCAAATAGAA
AAGCCGGGTGGCTATAATGAGTTAGAAAATAAAGAGGTCCCATTTGAATA
TTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTG
ATGACTTTATTATCGGAGCAATGGATACTAAAGAATTAAAAGAATTAAAA
GAATTAAAAAAATTAAAAGTAAAAAGTTATTTATTAAAACATCCGGAAAC
TGAGTTGAAAGATATAACATATGAATTGCCGGCACAGTCGAAGCTTATTA
AAAAA

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PRETTY of: /biotmp/msa212269.2{*}   February 10, 2003 05:07  ..

                             1                                                  50
   msa212269.2{184_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa212269.2{184_2603}   atgaaaaaac aaaaactatt actgcttatt ggaggcttat taataatgat
msa212269.2{184_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
              Consensus   ********** ********** ********** ********** **********

                          51                                                100
   msa212269.2{184_090}   ~~~~~~~~~~ ~~~~~TAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG
  msa212269.2{184_2603}   aatgatgaca gcatgTAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG
msa212269.2{184_18RS21}   ~~~~~~~~~~ ~~~~~TAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG
              Consensus   ********** ********** ********** ********** **********

                          101                                               150
   msa212269.2{184_090}   AAGAGTACCA AGCTGAACAA AATTTTAAAC tGTTTTTTGA GTTTTTAGCA
  msa212269.2{184_2603}   AAGAGTACCA AGCTGAACAA AATTTTAAAC cGTTTTTTGA GTTTTTAGCA
msa212269.2{184_18RS21}   AAGAGTACCA AGCTGAACAA AATTTTAAAC cGTTTTTTGA GTTTTTAGCA
              Consensus   ********** ********** ********** _********* **********

                          151                                               200
   msa212269.2{184_090}   CAAAAAtATA AAGATTTGAa CAAAATACAA AAATACTTAC TATTAGTATC
  msa212269.2{184_2603}   CAAAAAgATA AAGATTTGAg CAAAATACAA AAATACTTAC TATTAGTATC
msa212269.2{184_18RS21}   CAAAAAgATA AAGATTTGAg CAAAATACAA AAATACTTAC TATTAGTATC
              Consensus   ******_*** *********_ ********** ********** **********

                          201                                               250
   msa212269.2{184_090}   GGATTCAGGT GATGCATTAG ATTTAGAATA TTTCTATAGT ATTCAAGATT
  msa212269.2{184_2603}   GGATTCAGGT GATGCATTAG ATTTAGAATA TTTCTATAGT ATTCAAGATT
msa212269.2{184_18RS21}   GGATTCAGGT GATGCATTAG ATTTAGAATA TTTCTATAGT ATTCAAGATT
              Consensus   ********** ********** ********** ********** **********

                          251                                               300
   msa212269.2{184_090}   TAAAAAAAAA TAAGGATTTA GGGAAGTTTG AAACAAGAAA AAGTCAAATA
  msa212269.2{184_2603}   TAAAAAAAAA TAAGGATTTA GGGAAGTTTG AAACAAGAAA AAGTCAAATA
msa212269.2{184_18RS21}   TAAAAAAAAA TAAGGATTTA GGGAAGTTTG AAACAAGAAA AAGTCAAATA
              Consensus   ********** ********** ********** ********** **********

                          301                                               350
   msa212269.2{184_090}   GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTTGA
  msa212269.2{184_2603}   GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTTGA
msa212269.2{184_18RS21}   GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTTGA
              Consensus   ********** ********** ********** ********** **********
```

Table 50: Comparative Sequences relating to SAG 1024

```
                          351                                                  400
   msa212269.2{184_090}   ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT
  msa212269.2{184_2603}   ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT
msa212269.2{184_18RS21}   ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT
              Consensus   ********** ********** ********** ********** **********

                          401                                                  450
   msa212269.2{184_090}   TTGATGACTT TATTATCGGA GCAATGGATA CT........ ..........
  msa212269.2{184_2603}   TTGATGACTT TATTATCGGA GCAATGGATA CT........ .aaagaatta
msa212269.2{184_18RS21}   TTGATGACTT TATTATCGGA GCAATGGATA CTaaagaatt aaaagaatta
              Consensus   ********** ********** ********** **-------- ----------

                          451                                                  500
   msa212269.2{184_090}   AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA
  msa212269.2{184_2603}   AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA
msa212269.2{184_18RS21}   AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTTATTAA AACATCCGGA
              Consensus   ********** ********** ********** ********** **********

                          501                                                  550
   msa212269.2{184_090}   AACTGAGTTG AAAGATATAA CATATGAATT GCCGaCACAG TCGAAGCTTA
  msa212269.2{184_2603}   AACTGAGTTG AAAGATATAA CATATGAATT GCCGaCACAG TCGAAGCTTA
msa212269.2{184_18RS21}   AACTGAGTTG AAAGATATAA CATATGAATT GCCGgCACAG TCGAAGCTTA
              Consensus   ********** ********** ********** ****-***** **********

                          551
   msa212269.2{184_090}   TTAAAAAA
  msa212269.2{184_2603}   TTAAAAAA
msa212269.2{184_18RS21}   TTAAAAAA
              Consensus   ********
```

SEQ ID NO. 5004
STRAIN 2603 frame: 1
MKKQKLLLLIGGLLIMIMMTACKDSKIPENRTKEEYQAEQNFKPFFEFLAQKDKDLSKIQ
KYLLLVSDSGDALDLEYFYSIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFK
NNIVYPKGKPNITFDDFIIGAMDTKELKELKKLKVKSYLLKHPETELKDITYELPTQSKL
IKK

SEQ ID NO. 5005
STRAIN 090 frame: 2
KDSKIPENRTKEEYQAEQNFKLFFEFLAQKYKDLNKIQKYLLLVSDSGDALDLEYFYSIQ
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM
DTKELKKLKVKSYLLKHPETELKDITYELPTQSKLIKK

SEQ ID NO. 5006
STRAIN 18RS21 frame: 2
KDSKIPENRTKEEYQAEQNFKPFFEFLAQKDKDLSKIQKYLLLVSDSGDALDLEYFYSIQ
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM
DTKELKELKELKKLKVKSYLLKHPETELKDITYELPAQSKLIKK

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PRETTY of: /biotmp/msa212547.2{*}   February 10, 2003 05:11  ..

                          1                                                    50
msa212547.2{184_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~KDSKIPEN RTKEEYQAEQ NFKpFFEFLA
  msa212547.2{184_2603}   mkkqkllllі ggllimimmt acKDSKIPEN RTKEEYQAEQ NFKpFFEFLA
   msa212547.2{184_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~KDSKIPEN RTKEEYQAEQ NFKlFFEFLA
              Consensus   ********** ********** ********** ********** ***-******

                          51                                                   100
msa212547.2{184_18RS21}   QKdKDLsKIQ KYLLLVSDSG DALDLEYFYS IQDLKKNKDL GKFETRKSQI
  msa212547.2{184_2603}   QKdKDLsKIQ KYLLLVSDSG DALDLEYFYS IQDLKKNKDL GKFETRKSQI
   msa212547.2{184_090}   QKyKDLnKIQ KYLLLVSDSG DALDLEYFYS IQDLKKNKDL GKFETRKSQI
              Consensus   **-***-*** ********** ********** ********** **********

                          101                                                  150
msa212547.2{184_18RS21}   EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDTkelkel
  msa212547.2{184_2603}   EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDT...kel
   msa212547.2{184_090}   EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDT......
              Consensus   ********** ********** ********** ********** ****------

                          151                                  186
msa212547.2{184_18RS21}   KELKKLKVKS YLLKHPETEL KDITYELPaQ SKLIKK
  msa212547.2{184_2603}   KELKKLKVKS YLLKHPETEL KDITYELPtQ SKLIKK
   msa212547.2{184_090}   KELKKLKVKS YLLKHPETEL KDITYELPtQ SKLIKK
              Consensus   ********** ********** ********-*
```

Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101
STRAIN 2603
ttgaataataaaggtgtcggtggcgatggtgtccaaatttatcaatacta
tatcaaaatggacaacaataaaccttacttaagtcccaaagataagacta
ctgtagagaagttagaagatcgctggaaaaaattactttcaaagttcag
gatactggcattggtttgaaagacgtttatcttcaatctgttaagtatgt
tggtggtggcaataataatttagaccttatcacacctccaggatttaaaa
aagaagataaaaaagttgaaaaaccaaaattagaccgtccaccaggaatt
gatttaccagcaccaacttcaatgagaagttttgattattcaaccccacc
gggaactaagccaagcaaacccaaagatagtttatcaactcctccaggtt
tcccagatttaaacacgccgccggatgaagcaccaaaggatagtaaaaaa
gacgctattgaagataaatcaggagcaattaaatatgctaagtctcttca
acttagctttgttgatggccctattttagctagcaaagtaaatggcaaaa
tattacaagtcgaatctgatggcaaattagtcattcctagaaatgctttg
tcagctaatcaatttgatgacactagtcttaaaatttatcgtaataataa
tcgcaataaagaaattactatcacaacagattatttgcagatacaaaat
atgtcaatatcacagcggttgactatttgagcaatactacttttgagcaa
ttagctactggtgaaacagtagattaccatgccattgtattttcaagctt
tgctgctattaaagacaagggtggtaagatttatgttaacgataaattgc
aagaaacttctcgtatagcgcttaaagataaatctgttaagattggtatt
gaattaccaaatgatgtcagacatattgatagtttatctgttcgtcgttt
gaatgaggttaaaactgttgataatatcttgaaaaatgatgaacaagaca
ttaatctcagcaaaacttaccaattaaaatacaacccgacaaatcgtcgt
ctagagtttactattaataacattaactcaagttcagaaatcatgaccac
tttcaaagatggaaagatgccagaattggttgaacaaaaagatgtttctt
tggatataaacgatatggacatgagtaagtttaaaactattcgacttgga
cgaaaggattctgaatttaagggacaacttattgcaaaaactggaacagt
tgaattagatatgtttttcaaacaatctcaagacccagcttcaattatta
aaaaaatataccttatccaaaatggtgttccaaatgaattgaaaaaattt
gactctagttttggtttaactgaaagtcagatagatggatactatattta
taaagatgcaattaaccttaaatttaaattaaccagtggtgcaagtctta
aagttgtttataaagggcaagaagatccatatagtcatcagaaagaagat
atgactaaaaaaggtgaacagctcagtcattcaactcaagccaatgaaaa
tacagcaaaagtaacctttgctaatattgactggtcacattatagtaagg
ttactgtgaatggaaaagaagttgttaaaggtagtgagttacctttaact
aaaggatggacaacatttgtattacataaaacagaaaattcattaaatgt
taaaagtttgattatggagacgggtagtgtaagtaagaaagttcaacaac
ttcctttaagtcctagattatctaaaaataagcatatgagggatatgcta
cttactatgcaaaaagattcagcgtattacgaaacaagtgacagtctagt
ccttcgaattaatctcactgcagatactaaacttaattttaatgctgtta
aaggagcgagtgctcttactgaaaatatgatgatgagacagtttgcagtt
gctggaccacaagatgatcctgttagtgaacataaatacccatcagtatt
tctcttaactcctgccttattggaaactgctagtgaggcaactctaaatg
gtaaggaaatcacagcatctggtattatcggtcacatcaaggatggtgat
aaaagcaagcatgttgaagtcaaaatggtgaatgaaaatggagacatgct
aggaaccccctgttattattcaaggtaaagacttgactaatcgaacaaaac
cattaatgagtggacgtagagtactttatgccggtaaacaatatgagttc
cgggctaaattaccacttagtcgttttaacacttggattagggttgaagt
ggtaacagaagcaggagagaaagcaagtattgttcgtcgcatgttctttg
accaatcagttccagagcttaacacagcagttgctaaacgtgatttgact
tctgatactgctcttatccacatcgttgccaaagatgactctctaaaact
aaaattatatcaagatgattcattacttgaatctgttgataaaaccggtc
tttatagttttagaaatggtgtagaaatcactaaagatatgacagtacca
ctagaatttggagataatattattaagttatctgctgttgacttatcaaa
ttatcgtcgtaatgagacccttcatatctatagaaaccgttttgatgtta
aagcaagccaaatgacagctgacaaaggagctaaagtaactgtggatatg
ttgatgaagcacttagttgttccagaaatggcaggagcttatacattaac
aatcgacgaagctccaaacacaaatgaatcaggaatgttaacaaacgcta
aagtatcgattcattatgtaaatggtggtgttgataaagttgatgttccg
attaaagtagttgacttagaagctattcgtaaagctgaagaagcacgtaa
agctgaagaagcacgtaaagctgaagaagcacgtaaagctgaagagggac
ataaaacccaagaagcacctatagttgaagaaggctacaaggttaataac
gttcatcaaactgatactacagttaaagcgtctgatttaccaaagactaa
gacagtttccgcagttcatatggctagaacagacaataaacagataactt
cacatcagacacatgttgaaaaacaaattaaaaatacattgccatccact
ggtgacagcaaacgtggttattatatcactggaatggctatcgttatgct
gagtgtattatttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102
STRAIN A909
TTGAATAATAAAGGTGTCGGTGGCGAT
GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA
CTTAAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA
AAAAAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTT
TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCT
TATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAA
AATTAGACCGTCCACCAGGAATTGATTTACCaCCACCAACTTCAATGAGA
AGTTTTGATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAGA
TAGTTTATCAACTCCTCCAGGTTTCCCAGATTTAAACACGCCGCCGGATG
AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA
ATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTT
AGCTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAT
TAGTCATTCCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAAC
AGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATT
TGAGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTAC
CATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAA
GATTTATGTTAACGATAAATTGCAAGAAACTTCTCGTATAGCGCTTAAAG
ATAAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATT
GATAGTTTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATAT
CTTGAAAAATGATGAACAAGACATTAATCTCAGCAAAACTTACCAATTAA
AATACAACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAAC
TCAAGTTCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATT
GGTTGAaCAAAAAGATGTTTCTTTGGATATAaaCGATATGGACATGAGTA
AGTTTAAAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAA
CTTATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATC
TCAAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGTG
TTCCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAGT
CAGATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAA
ATTAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATC
CATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGT
CATTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATAT
TGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTA
AAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACAT
AAAACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTAG
TGTAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCTAAAA
ATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTAT
TACGAaaCAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATAC
TAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATA
TGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGT
GAACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAAAC
TGCTAGTGAGGCAACTCTaAATGGTAAGGAAATCACAGCATCTGGTATTA
TCGGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATG
GTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAA
AGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTT
ATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTT
AACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAG
TATTGTTCGTCGCATGTTCTTTGACCAATCAGtTCCAGAGCTTAACACAG
CAGTTGCTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTT
GCCAAAGATGACTCTCTAAAACTAAAATTATATCAAGATGATTCATTACT
TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAA
TCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAG
TTATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATAT
CTATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAG
GAGCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAA
ATGGCAGGAGCTTATACATTAACAATCGACGAAGATCCAAACACAAATGA
ATCAGGAATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGTG
GTGTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATT
CGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGA
AGCACGTAAAGCTGAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTG
AAGAGGGACATaAAACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAG
GTTAATAACGTTCATCAAACTGATACTACAGTTAAAGCGTCTGATTTACC
AAAGACTAAGACAGTTTCCGCAGTTCATATGGCTAGAACAGACAATAAAC
AGATAACTTCACATCAGACACATGTTGAAAAACAAATTAAAAATA

SEQ ID NO. 5103
STRAIN H36B
TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTT
ACTTAAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG
AAAAAAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGT
TTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACC
TTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCA
AAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAG
AAGTTTTGATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAG
ATAGTTTATCAACTCCTCCAGGTTTCCCAGATTTAAACACGCCGCCGGAT
GAAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGC
AATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTT
TAGCTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAA
TTAGTCATTCCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAG
TCTTAAAATTTATCGTAATAATAATCGCAATAAAGAAATTacTATCACAA
CAGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTAT
TTGAGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAaCAGTAGATTA
CCATGCCATTGTAtTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTA
AGATTTATGTCAACGATAAATTGCAAGAAACTTCTCGTATAGCGCTTAAA
GATAAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATAT
TGATAGTTTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATA
TCTTGAAAAATGATGAACAAGACATTAATCTCAGCAAAACTTACCAATTA
AAATACAACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAA
CTCAAGTTCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAgAAT
TGGTTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGT
AAGTTTAAAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACA
ACTTATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAAT
CTCAAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGT
GTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAG
TCAGATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTA
AATTAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGtCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAG
TCATTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATA
TTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGT
AAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACA
TAAAACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTA
GTGTAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCTAAA
AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTA
TTACGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATA
CTAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAAT
ATGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAG
TGAACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAAA
CTGCTAGTGAGGCaACTCTAAATGGTAAGGAAATCACAGCATCTGGTATT
ATCGGTCACATCAAGGATGGtGATAAAAGCAAGCATGTTGAAGTCAAAAT
GGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTA
AAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTT
TATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTT
TAACaCTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAA
GTATTGTTCGTCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACA
GCAGTTGCTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGT
TGCCAAAGATGACTCTCTAAAACTAAAATTATATCAAGATGATTCATTAC
TTGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAA
ATCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTACTAA
GTTATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATA
TCTATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAA
GGAGCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGA
AATGGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATG
AATCAGGAATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGT
GGTGTTGATAAAGttGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTAT
TCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAG
AAGCACGTAAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAAGCT
GAAGAAGCACATAAAGTCGAAGAAGCACGTAAAGCTGAAGAGGGACATAA
AACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAACGTTC
ATCAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACA
GTTTCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACA
TCAGACACATG

SEQ ID NO. 5104
STRAIN 18RS21
TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCCAA
ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGTCC
CAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAATTA
CTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTATCTTCAA
TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC
TCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAATTAGACC
GTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGTTTTGAT
TATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAGATAGTTTATC
AACTCCTCCAGGTTTCCCAGATTTAAACACGCCGCCGGaTGAAGCACCAA
AGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAATAT
GCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTTAGCTAGCAA
AGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTAGTCATTC
CTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAAATT
TATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAGATTATTT
TGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCAATA
CTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCATGCCATT
GTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTATGT
TAACGATAAATTGCAAGAaACTTCTCGTATAGCGCTTAAAGATAAATCTG
TTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGATAGTTTA
TCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATATCTTGAAAAA
TGATGAACAAGACATTAATCTCAGCAAaACTTACCAATTAAAATACAACC
CGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTCAAGTTCA
GAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATTGGTTGAACA
AAAAGATGTTTCTTTGGATATaAACGATATGGACATGAGTAAGTTTAAAA
CTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACTTATTGCA
AAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTCAAGACCC
AGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGTGTTCCAAATG
AATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAGTCAGATAGAT
GGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAACCAG
TGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATAGTC
ATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT
CAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC
ACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGTTAAAGGTAGTG
AGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACAGAA
AATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTAGTGTAAGTAA
GAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCTAAAAATAAGCATA
TGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTATTACGAAACA
AGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATACTAAACTTAA
TTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATGATGATGA
GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA
TACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAAACTGCTAGTGA
GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCACA
TCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGTGAATGAA
AATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAGACTTGAC
TAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA

Table 51: Comparative Sequences relating to SAG0677

AACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAACACTTGG
ATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCG
TCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCAGTTGCTA
AACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAAGAT
GACTCTCTAAAACTAAAATTATATCAAGATGATTCATTACtTGAATCTGT
TGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATCACTAAAG
ATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAGTTATCTGCT
GTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCTATAGAAA
CCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG
TAACTGTGGaTATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA
GCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT
GTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGTGGTGTTGATA
AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCGTAAAGCT
GAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTGAAGAGGGACATAA
AACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAACGTTC
ATCAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACA
GTTTCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACA
TCAGACACATGTTGAA

SEQ ID NO. 5105
STRAIN M732
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CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAAT
TACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTATCTTC
AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA
CCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAATTAGA
CCGTCCacCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGTTTTG
ATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAGATAGTTTA
TCAACTCCTCCAGGTTTCCCAGATTTAAACACGCCGCCGGATGAAGCCAC
CAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAA
TATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTTAGCTAG
CAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTAGTCA
TTCCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAA
ATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAGATTA
TTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCA
ATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCATGCC
ATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTA
TGTTAACGATAAATTGCAAGAAACTTCTCGTATAGCGCTTAAAGATAAAT
CTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGATAGT
TTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATATCTTGAA
AAATGATGAACAAGACATTAATCTCAGCAAAACTTACCAATTAAAATACA
ACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTCAAGT
TCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATTGGTTGA
ACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAGTTTA
AAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACTTATT
GCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTCAAGA
CCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGtGTTCCAA
ATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAGTCAGATA
GATGGATACTATATTTATAAAGATGCAATTAACCTTAAaTTTAAATTAAC
CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA
GTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCA
ACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG
GTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTAAAGGTA
GTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACA
GAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTAGTGTAAG
TAAGAAAGTTCAACAACTTcCTTTAAGTCCTAGATTATCTAAAAATAAGC
ATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTATTACGAA
ACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATACTAAACT
TAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATGATGA
TGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTaGTGAACAT
AAATACCCATCAGTaTTTCTCTTAACTCCTGCCTTATTGGAAaCTGCTAG
TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC
ACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGTGAAT
GAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAGACTT
GACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCG
GTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGtCGTTTTAACACT
TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT
TCGTCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCAGTTG
CTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAA
GATGACTCTCTAAAACTAAAATTATATCAAGATGATTCATTACTTGAATC
TGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATCACTA
AAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAGTTATCT
GCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCTATAG
AAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA
AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA
GGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGG
AATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGTGGTGTTG
ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCGTAAA
GCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAGCACG
TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAAGAAG
CACATAAAGTCGAAGAAGCACGTAAAGCTGAAGAGGGACATAAAACCCAA
GAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTCATCAAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGTTTCCG
CAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCAGACA
CATGTTGAAAA

SEQ ID NO. 5106
STRAIN COH1
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GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAGATAG
TTTATCAACTCCTCCAGGtTTCCCAGATTTAAACACGCCGCCGGATGAAG
CCaCCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTTAG
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTA
GTCATTCCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCT
TAAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAG
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AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA
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AAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGA
TAGTTTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAATCTCAGCAAAACTTACCAATTAAAA
TACAACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTC
AAGTTCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATTGG
TTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACT
TATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTC
AAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGTGTT
CCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAGTCA
GATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA
AACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTAGTG
TAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAgATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTATTA
CGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATACTA
AACTTAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATG
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ACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGT
GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA
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GTTGCTAAACGTGATTtGACTTCTGATACTGCTCTTATCCACATCGTTGC
CAAAGATGACTCTCTAAAaCTAAAATTATATCAAGATGATTCATTACTTG
AATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATC
ACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAGTT
ATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCT
ATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA
GCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAAT
CAGGAATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAG
CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
GAAGCACATAAAGTCGAAGAAGCACGTAAAGCTGAAGAGGGACATAAAAC
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTCATC
AAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGTT
TCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCA
GACACATGT

SEQ ID NO. 5107
STRAIN M781
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AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCAAAGATAG
TTTATCAACTCCTCCAGGTTTCCCAGATTTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCTATTTTAG
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTA
GTCATTCCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCT
TAAaATTTATCGTAATAATAATCGCAATAAAGAAATTaCTATCACAACAG
ATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTG
AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA
TTTATGTTAACGATAAATTGCAAGAAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACATATTGA
TAGTTTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAATCTCAGCAAAACTTACCAATTAAAA
TACAACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTC
AAGTTCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAGAATTGG
TTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACT
TATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAACAATCTC
AAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAATGGTGTT
CCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGAAAGTCA
GATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA
AACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGGGTAGTG
TAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGCGTATTA
CGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATACTA
AACTTAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATATG
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ACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGGAAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGT
GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA
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GTTGCTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGC
CAAAGATGACTCTCTAAAACTAAAATTATATCAAGATGATTCATTACTTG
AATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAATC
ACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAGTT
ATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTCATATCT
ATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA
GCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAAT
CAGGAATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGAAG
CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
GAAGCACATAAAGTCGAAGAAGCACCGTAAAGCTGAAGAGGGACATAAAA
CCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTCAT
CAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGT
TTCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATC
AGACACATGTTG

SEQ ID NO. 5109
STRAIN JM9130013
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CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAG
ACCTTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAA
CCAAAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAAT
GAGAAGTTTTGATTATTCAACCCCACCGGGAACTAAGCCAAGCAAACCCA
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GATGAAGCACCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG
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TTTTAGCTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGC
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AAAGATAAATCTGTTAAGATTGGTATTGAATTACCAAATGATGTCAGACA
TATTGATAGTTTATCTGTTCGTCGTTTGAATGAGGTTAAAACTGTTGATA
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TTAAAATACAACCCGACAAATCGTCGTCTAGAGTTTACTATTAATAACAT
TAACTCAAGTTCAGAAATCATGACCACTTTCAAAGATGGAAAGATGCCAG
AATTGGTTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATG
AGTAAGTTTAAAACTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGG

Table 51: Comparative Sequences relating to SAG0677

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ACAACTTATTGCAAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAAC
AATCTCAAGACCCAGCTTCAATTATTAAAAAAATATACCTTATCCAAAAT
GGTGTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTTGGTTTAACTGA
AAGTCAGATAGATGGATACTATATTTATAAAGATGCAATTAACCTTAAAT
TTAAATTAACCAGTGGTGCAaGTCTTAAAGTTGTTTATAAAGGGCAAGAA
GATCCATATAGTCATCAGAAAGAAGATATGACTAAAArAGGTGAACAGCT
CAGTCATTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTA
ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTT
GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATT
ACATAAAACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGG
GTAGTGTAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCT
AAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTCAGC
GTATTACGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAG
ATACTAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAA
AATATGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGT
TAGTGAACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGG
AAACTGCTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT
ATTATCGGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAA
AATGGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAG
GTAAAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTA
CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCG
TTTTAACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAgaGaaag
cAaGTATTGTTCGTCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAAC
ACAGCAGTTGCTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACAT
CGTTGCCAAAGATGACTCTCTAAAACTAAAATTATATCAAGATGATTCAT
TACTTGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTA
GAAATCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTAT
TAAGTTATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCTTC
ATATCTATAGAAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGAC
AAAGGAGCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCC
AGAAATGGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAA
ATGAATCAGGAATGTTAACAAACGCTAAAGTATCGATTCATTATGTAAAT
GGTGGTGTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGC
TATTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTG
AAGAAGCACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAA
GCTGAAGAAGCACATAAAGTCGAAGAAGCACCGTAAAGCTGAAGAGGGAC
ATAAAACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGGTTAATAAC
GTTCATCAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAA
GACAGTTTCCGCAGTTCATATGGCTAGAACAGACAATAAACAGATAACTT
CACATCAGACACATGTTG
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         msa235280.2{195_M732}  ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
         msa235280.2{195_M781}  ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
         msa235280.2{195_H36B}  ---------- ---------- ------TGGT GTCCAAATTT ATCAATACTA
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         msa235280.2{195_2603}  ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
         msa235280.2{195_A909}  ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
                     Consensus  ---------- ---------- ------**** ********** **********

                                51                                              100
         msa235280.2{195_COH1}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
         msa235280.2{195_M732}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
         msa235280.2{195_M781}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
         msa235280.2{195_H36B}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
     msa235280.2{195_JM9130013}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
       msa235280.2{195_18RS21}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
         msa235280.2{195_2603}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
         msa235280.2{195_A909}  TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAAA GATAAGACTA
                     Consensus  ********** ********** ********** ********** **********

                                101                                             150
         msa235280.2{195_COH1}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
         msa235280.2{195_M732}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
         msa235280.2{195_M781}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
         msa235280.2{195_H36B}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
     msa235280.2{195_JM9130013}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
       msa235280.2{195_18RS21}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
         msa235280.2{195_2603}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
         msa235280.2{195_A909}  CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
                     Consensus  ********** ********** ********** ********** **********

                                151                                             200
         msa235280.2{195_COH1}  GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
         msa235280.2{195_M732}  GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
         msa235280.2{195_M781}  GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
         msa235280.2{195_H36B}  GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
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Table 51: Comparative Sequences relating to SAG0677

```
msa235280.2{195_JM9130013}  GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
  msa235280.2{195_18RS21}   GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
    msa235280.2{195_2603}   GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
    msa235280.2{195_A909}   GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
                Consensus   ********** ********** ********** ********** **********

                            201                                              250
    msa235280.2{195_COH1}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
    msa235280.2{195_M732}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
    msa235280.2{195_M781}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
    msa235280.2{195_H36B}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
msa235280.2{195_JM9130013}  TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
  msa235280.2{195_18RS21}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
    msa235280.2{195_2603}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
    msa235280.2{195_A909}   TGGTGGTGGC AATAATAATT TAGACCTTAT CACACCTCCA GGATTTAAAA
                Consensus   ********** ********** ********** ********** **********

                            251                                              300
    msa235280.2{195_COH1}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
    msa235280.2{195_M732}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
    msa235280.2{195_M781}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
    msa235280.2{195_H36B}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
msa235280.2{195_JM9130013}  AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
  msa235280.2{195_18RS21}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
    msa235280.2{195_2603}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
    msa235280.2{195_A909}   AAGAAGATAA AAAAGTTGAA AAACCAAAAT TAGACCGTCC ACCAGGAATT
                Consensus   ********** ********** ********** ********** **********

                            301                                              350
    msa235280.2{195_COH1}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
    msa235280.2{195_M732}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
    msa235280.2{195_M781}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
    msa235280.2{195_H36B}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
msa235280.2{195_JM9130013}  GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
  msa235280.2{195_18RS21}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
    msa235280.2{195_2603}   GATTTACCAg CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
    msa235280.2{195_A909}   GATTTACCAc CACCAACTTC AATGAGAAGT TTTGATTATT CAACCCCACC
                Consensus   *********_ ********** ********** ********** **********

                            351                                              400
    msa235280.2{195_COH1}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
    msa235280.2{195_M732}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
    msa235280.2{195_M781}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
    msa235280.2{195_H36B}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
msa235280.2{195_JM9130013}  GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
  msa235280.2{195_18RS21}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
    msa235280.2{195_2603}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
    msa235280.2{195_A909}   GGGAACTAAG CCAAGCAAAC CCAAAGATAG TTTATCAACT CCTCCAGGTT
                Consensus   ********** ********** ********** ********** **********

                            401                                              450
    msa235280.2{195_COH1}   TCCCAGATTT AAACACGCCG CCGGATGAAG cCACcAAAGG ATAGTAAAAA
    msa235280.2{195_M732}   TCCCAGATTT AAACACGCCG CCGGATGAAG cCACcAAAGG ATAGTAAAAA
    msa235280.2{195_M781}   TCCCAGATTT AAACACGCCG CCGGATGAAG cCACcAAAGG ATAGTAAAAA
    msa235280.2{195_H36B}   TCCCAGATTT AAACACGCCG CCGGATGAAG .CACtAAAGG ATAGTAAAAA
msa235280.2{195_JM9130013}  TCCCAGATTT AAACACGCCG CCGGATGAAG .CACcAAAGG ATAGTAAAAA
  msa235280.2{195_18RS21}   TCCCAGATTT AAACACGCCG CCGGATGAAG .CACcAAAGG ATAGTAAAAA
    msa235280.2{195_2603}   TCCCAGATTT AAACACGCCG CCGGATGAAG .CACcAAAGG ATAGTAAAAA
    msa235280.2{195_A909}   TCCCAGATTT AAACACGCCG CCGGATGAAG .CACtAAAGG ATAGTAAAAA
                Consensus   ********** ********** ********** _***_***** **********

                            451                                              500
    msa235280.2{195_COH1}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
    msa235280.2{195_M732}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
    msa235280.2{195_M781}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
    msa235280.2{195_H36B}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
msa235280.2{195_JM9130013}  AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
  msa235280.2{195_18RS21}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
    msa235280.2{195_2603}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
    msa235280.2{195_A909}   AGACGCTATT GAAGATAAAT CAGGAGCAAT TAAATATGCT AAGTCTCTTC
                Consensus   ********** ********** ********** ********** **********

                            501                                              550
    msa235280.2{195_COH1}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
    msa235280.2{195_M732}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
    msa235280.2{195_M781}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
    msa235280.2{195_H36B}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
msa235280.2{195_JM9130013}  AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
  msa235280.2{195_18RS21}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
    msa235280.2{195_2603}   AACTTAGCTT TGTTGATGgC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
    msa235280.2{195_A909}   AACTTAGCTT TGTTGATGaC CCTATTTTAG CTAGCAAAGT AAATGGCAAA
                Consensus   ********** ********_* ********** ********** **********
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Table 51: Comparative Sequences relating to SAG0677

```
                              551                                                 600
     msa235280.2{195_COH1}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
     msa235280.2{195_M732}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
     msa235280.2{195_M781}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
     msa235280.2{195_H36B}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
msa235280.2{195_JM9130013}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
   msa235280.2{195_18RS21}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
     msa235280.2{195_2603}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
     msa235280.2{195_A909}    ATATTACAAG TCGAATCTGA TGGCAAATTA GTCATTCCTA GAAATGCTTT
                 Consensus    ********** ********** ********** ********** **********

                              601                                                 650
     msa235280.2{195_COH1}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
     msa235280.2{195_M732}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
     msa235280.2{195_M781}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
     msa235280.2{195_H36B}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
msa235280.2{195_JM9130013}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
   msa235280.2{195_18RS21}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
     msa235280.2{195_2603}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
     msa235280.2{195_A909}    GTCAGCTAAT CAATTTGATG ACACTAGTCT TAAAATTTAT CGTAATAATA
                 Consensus    ********** ********** ********** ********** **********

                              651                                                 700
     msa235280.2{195_COH1}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
     msa235280.2{195_M732}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
     msa235280.2{195_M781}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
     msa235280.2{195_H36B}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
msa235280.2{195_JM9130013}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
   msa235280.2{195_18RS21}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
     msa235280.2{195_2603}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
     msa235280.2{195_A909}    ATCGCAATAA AGAAATTACT ATCACAACAG ATTATTTTGC AGATACAAAA
                 Consensus    ********** ********** ********** ********** **********

                              701                                                 750
     msa235280.2{195_COH1}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
     msa235280.2{195_M732}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
     msa235280.2{195_M781}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
     msa235280.2{195_H36B}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
msa235280.2{195_JM9130013}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
   msa235280.2{195_18RS21}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
     msa235280.2{195_2603}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
     msa235280.2{195_A909}    TATGTCAATA TCACAGCGGT TGACTATTTG AGCAATACTA CTTTTGAGCA
                 Consensus    ********** ********** ********** ********** **********

                              751                                                 800
     msa235280.2{195_COH1}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
     msa235280.2{195_M732}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
     msa235280.2{195_M781}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
     msa235280.2{195_H36B}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
msa235280.2{195_JM9130013}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
   msa235280.2{195_18RS21}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
     msa235280.2{195_2603}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
     msa235280.2{195_A909}    ATTAGCTACT GGTGAAACAG TAGATTACCA TGCCATTGTA TTTTCAAGCT
                 Consensus    ********** ********** ********** ********** **********

                              801                                                 850
     msa235280.2{195_COH1}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
     msa235280.2{195_M732}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
     msa235280.2{195_M781}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
     msa235280.2{195_H36B}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTcAA CGATAAATTG
msa235280.2{195_JM9130013}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
   msa235280.2{195_18RS21}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
     msa235280.2{195_2603}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
     msa235280.2{195_A909}    TTGCTGCTAT TAAAGACAAG GGTGGTAAGA TTTATGTtAA CGATAAATTG
                 Consensus    ********** ********** ********** *******-** **********

                              851                                                 900
     msa235280.2{195_COH1}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
     msa235280.2{195_M732}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
     msa235280.2{195_M781}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
     msa235280.2{195_H36B}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
msa235280.2{195_JM9130013}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
   msa235280.2{195_18RS21}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
     msa235280.2{195_2603}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
     msa235280.2{195_A909}    CAAGAAACTT CTCGTATAGC GCTTAAAGAT AAATCTGTTA AGATTGGTAT
                 Consensus    ********** ********** ********** ********** **********

                              901                                                 950
     msa235280.2{195_COH1}    TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
     msa235280.2{195_M732}    TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
     msa235280.2{195_M781}    TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
     msa235280.2{195_H36B}    TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
msa235280.2{195_JM9130013}    TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
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Table 51: Comparative Sequences relating to SAG0677

```
   msa235280.2{195_18RS21}  TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
     msa235280.2{195_2603}  TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
     msa235280.2{195_A909}  TGAATTACCA AATGATGTCA GACATATTGA TAGTTTATCT GTTCGTCGTT
                 Consensus  ********** ********** ********** ********** **********

                            951                                              1000
     msa235280.2{195_COH1}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
     msa235280.2{195_M732}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
     msa235280.2{195_M781}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
     msa235280.2{195_H36B}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
msa235280.2{195_JM9130013}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
   msa235280.2{195_18RS21}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
     msa235280.2{195_2603}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
     msa235280.2{195_A909}  TGAATGAGGT TAAAACTGTT GATAATATCT TGAAAAATGA TGAACAAGAC
                 Consensus  ********** ********** ********** ********** **********

                            1001                                             1050
     msa235280.2{195_COH1}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
     msa235280.2{195_M732}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
     msa235280.2{195_M781}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
     msa235280.2{195_H36B}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
msa235280.2{195_JM9130013}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
   msa235280.2{195_18RS21}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
     msa235280.2{195_2603}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
     msa235280.2{195_A909}  ATTAATCTCA GCAAAACTTA CCAATTAAAA TACAACCCGA CAAATCGTCG
                 Consensus  ********** ********** ********** ********** **********

                            1051                                             1100
     msa235280.2{195_COH1}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
     msa235280.2{195_M732}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
     msa235280.2{195_M781}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
     msa235280.2{195_H36B}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
msa235280.2{195_JM9130013}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
   msa235280.2{195_18RS21}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
     msa235280.2{195_2603}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
     msa235280.2{195_A909}  TCTAGAGTTT ACTATTAATA ACATTAACTC AAGTTCAGAA ATCATGACCA
                 Consensus  ********** ********** ********** ********** **********

                            1101                                             1150
     msa235280.2{195_COH1}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
     msa235280.2{195_M732}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
     msa235280.2{195_M781}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
     msa235280.2{195_H36B}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
msa235280.2{195_JM9130013}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
   msa235280.2{195_18RS21}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
     msa235280.2{195_2603}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
     msa235280.2{195_A909}  CTTTCAAAGA TGGAAAGATG CCAGAATTGG TTGAACAAAA AGATGTTTCT
                 Consensus  ********** ********** ********** ********** **********

                            1151                                             1200
     msa235280.2{195_COH1}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
     msa235280.2{195_M732}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
     msa235280.2{195_M781}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
     msa235280.2{195_H36B}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
msa235280.2{195_JM9130013}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
   msa235280.2{195_18RS21}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
     msa235280.2{195_2603}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
     msa235280.2{195_A909}  TTGGATATAA ACGATATGGA CATGAGTAAG TTTAAAACTA TTCGACTTGG
                 Consensus  ********** ********** ********** ********** **********

                            1201                                             1250
     msa235280.2{195_COH1}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
     msa235280.2{195_M732}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
     msa235280.2{195_M781}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
     msa235280.2{195_H36B}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
msa235280.2{195_JM9130013}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
   msa235280.2{195_18RS21}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
     msa235280.2{195_2603}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
     msa235280.2{195_A909}  ACGAAAGGAT TCTGAATTTA AGGGACAACT TATTGCAAAA ACTGGAACAG
                 Consensus  ********** ********** ********** ********** **********

                            1251                                             1300
     msa235280.2{195_COH1}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
     msa235280.2{195_M732}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
     msa235280.2{195_M781}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
     msa235280.2{195_H36B}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
msa235280.2{195_JM9130013}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
   msa235280.2{195_18RS21}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
     msa235280.2{195_2603}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
     msa235280.2{195_A909}  TTGAATTAGA TATGTTTTTC AAACAATCTC AAGACCCAGC TTCAATTATT
                 Consensus  ********** ********** ********** ********** **********

                            1301                                             1350
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Table 51: Comparative Sequences relating to SAG0677

```
      msa235280.2{195_COH1}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
      msa235280.2{195_M732}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
      msa235280.2{195_M781}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
      msa235280.2{195_H36B}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
  msa235280.2{195_JM9130013} AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
     msa235280.2{195_18RS21} AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
      msa235280.2{195_2603}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
      msa235280.2{195_A909}  AAAAAAATAT ACCTTATCCA AAATGGTGTT CCAAATGAAT TGAAAAAATT
                 Consensus   ********** ********** ********** ********** **********

                             1351                                              1400
      msa235280.2{195_COH1}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
      msa235280.2{195_M732}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
      msa235280.2{195_M781}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
      msa235280.2{195_H36B}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
  msa235280.2{195_JM9130013} TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
     msa235280.2{195_18RS21} TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
      msa235280.2{195_2603}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
      msa235280.2{195_A909}  TGACTCTAGT TTTGGTTTAA CTGAAAGTCA GATAGATGGA TACTATATTT
                 Consensus   ********** ********** ********** ********** **********

                             1401                                              1450
      msa235280.2{195_COH1}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
      msa235280.2{195_M732}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
      msa235280.2{195_M781}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
      msa235280.2{195_H36B}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
  msa235280.2{195_JM9130013} ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
     msa235280.2{195_18RS21} ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
      msa235280.2{195_2603}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
      msa235280.2{195_A909}  ATAAAGATGC AATTAACCTT AAATTTAAAT TAACCAGTGG TGCAAGTCTT
                 Consensus   ********** ********** ********** ********** **********

                             1451                                              1500
      msa235280.2{195_COH1}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
      msa235280.2{195_M732}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
      msa235280.2{195_M781}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
      msa235280.2{195_H36B}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
  msa235280.2{195_JM9130013} AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
     msa235280.2{195_18RS21} AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
      msa235280.2{195_2603}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
      msa235280.2{195_A909}  AAAGTTGTTT ATAAAGGGCA AGAAGATCCA TATAGTCATC AGAAAGAAGA
                 Consensus   ********** ********** ********** ********** **********

                             1501                                              1550
      msa235280.2{195_COH1}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
      msa235280.2{195_M732}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
      msa235280.2{195_M781}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
      msa235280.2{195_H36B}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
  msa235280.2{195_JM9130013} TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
     msa235280.2{195_18RS21} TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
      msa235280.2{195_2603}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
      msa235280.2{195_A909}  TATGACTAAA AaAGGTGAAC AGCTCAGTCA TTCAACTCAA GCCAATGAAA
                 Consensus   ********** *_******** ********** ********** **********

                             1551                                              1600
      msa235280.2{195_COH1}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
      msa235280.2{195_M732}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
      msa235280.2{195_M781}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
      msa235280.2{195_H36B}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
  msa235280.2{195_JM9130013} ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
     msa235280.2{195_18RS21} ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
      msa235280.2{195_2603}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
      msa235280.2{195_A909}  ATACAGCAAA AGTAACCTTT GCTAATATTG ACTGGTCACA TTATAGTAAG
                 Consensus   ********** ********** ********** ********** **********

                             1601                                              1650
      msa235280.2{195_COH1}  GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
      msa235280.2{195_M732}  GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
      msa235280.2{195_M781}  GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
      msa235280.2{195_H36B}  GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
  msa235280.2{195_JM9130013} GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
     msa235280.2{195_18RS21} GTTACTGTGA ATGGAAAAGA AGTTGtTAAA GGTAGTGAGT TACCTTTAAC
      msa235280.2{195_2603}  GTTACTGTGA ATGGAAAAGA AGTTGtTAAA GGTAGTGAGT TACCTTTAAC
      msa235280.2{195_A909}  GTTACTGTGA ATGGAAAAGA AGTTGgTAAA GGTAGTGAGT TACCTTTAAC
                 Consensus   ********** ********** *****_**** ********** **********

                             1651                                              1700
      msa235280.2{195_COH1}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
      msa235280.2{195_M732}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
      msa235280.2{195_M781}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
      msa235280.2{195_H36B}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
  msa235280.2{195_JM9130013} TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
     msa235280.2{195_18RS21} TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
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Table 51: Comparative Sequences relating to SAG0677

```
     msa235280.2{195_2603}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
     msa235280.2{195_A909}  TAAAGGATGG ACAACATTTG TATTACATAA AACAGAAAAT TCATTAAATG
                 Consensus  ********** ********** ********** ********** **********

                            1701                                               1750
     msa235280.2{195_COH1}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
     msa235280.2{195_M732}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
     msa235280.2{195_M781}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
     msa235280.2{195_H36B}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
msa235280.2{195_JM9130013}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
   msa235280.2{195_18RS21}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
     msa235280.2{195_2603}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
     msa235280.2{195_A909}  TTAAAAGTTT GATTATGGAG ACGGGTAGTG TAAGTAAGAA AGTTCAACAA
                 Consensus  ********** ********** ********** ********** **********

                            1751                                               1800
     msa235280.2{195_COH1}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
     msa235280.2{195_M732}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
     msa235280.2{195_M781}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
     msa235280.2{195_H36B}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
msa235280.2{195_JM9130013}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
   msa235280.2{195_18RS21}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
     msa235280.2{195_2603}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
     msa235280.2{195_A909}  CTTCCTTTAA GTCCTAGATT ATCTAAAAAT AAGCATATGA GGGATATGCT
                 Consensus  ********** ********** ********** ********** **********

                            1801                                               1850
     msa235280.2{195_COH1}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
     msa235280.2{195_M732}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
     msa235280.2{195_M781}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
     msa235280.2{195_H36B}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
msa235280.2{195_JM9130013}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
   msa235280.2{195_18RS21}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
     msa235280.2{195_2603}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
     msa235280.2{195_A909}  ACTTACTATG CAAAAAGATT CAGCGTATTA CGAAACAAGT GACAGTCTAG
                 Consensus  ********** ********** ********** ********** **********

                            1851                                               1900
     msa235280.2{195_COH1}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
     msa235280.2{195_M732}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
     msa235280.2{195_M781}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
     msa235280.2{195_H36B}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
msa235280.2{195_JM9130013}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
   msa235280.2{195_18RS21}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
     msa235280.2{195_2603}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
     msa235280.2{195_A909}  TCCTTCGAAT TAATCTCACT GCAGATACTA AACTTAATTT TAATGCTGTT
                 Consensus  ********** ********** ********** ********** **********

                            1901                                               1950
     msa235280.2{195_COH1}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
     msa235280.2{195_M732}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
     msa235280.2{195_M781}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
     msa235280.2{195_H36B}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
msa235280.2{195_JM9130013}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
   msa235280.2{195_18RS21}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
     msa235280.2{195_2603}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
     msa235280.2{195_A909}  AAAGGAGCGA GTGCTCTTAC TGAAAATATG ATGATGAGAC AGTTTGCAGT
                 Consensus  ********** ********** ********** ********** **********

                            1951                                               2000
     msa235280.2{195_COH1}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
     msa235280.2{195_M732}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
     msa235280.2{195_M781}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
     msa235280.2{195_H36B}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
msa235280.2{195_JM9130013}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
   msa235280.2{195_18RS21}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
     msa235280.2{195_2603}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
     msa235280.2{195_A909}  TGCTGGACCA CAAGATGATC CTGTTAGTGA ACATAAATAC CCATCAGTAT
                 Consensus  ********** ********** ********** ********** **********

                            2001                                               2050
     msa235280.2{195_COH1}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
     msa235280.2{195_M732}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
     msa235280.2{195_M781}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
     msa235280.2{195_H36B}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
msa235280.2{195_JM9130013}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
   msa235280.2{195_18RS21}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
     msa235280.2{195_2603}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
     msa235280.2{195_A909}  TTCTCTTAAC TCCTGCCTTA TTGGAAACTG CTAGTGAGGC AACTCTAAAT
                 Consensus  ********** ********** ********** ********** **********

                            2051                                               2100
     msa235280.2{195_COH1}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
```

Table 51: Comparative Sequences relating to SAG0677

```
     msa235280.2{195_M732}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
     msa235280.2{195_M781}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
     msa235280.2{195_H36B}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
msa235280.2{195_JM9130013}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
   msa235280.2{195_18RS21}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
     msa235280.2{195_2603}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
     msa235280.2{195_A909}  GGTAAGGAAA TCACAGCATC TGGTATTATC GGTCACATCA AGGATGGTGA
                 Consensus  ********** ********** ********** ********** **********

                            2101                                               2150
     msa235280.2{195_COH1}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
     msa235280.2{195_M732}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
     msa235280.2{195_M781}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
     msa235280.2{195_H36B}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
msa235280.2{195_JM9130013}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
   msa235280.2{195_18RS21}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
     msa235280.2{195_2603}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
     msa235280.2{195_A909}  TAAAAGCAAG CATGTTGAAG TCAAAATGGT GAATGAAAAT GGAGACATGC
                 Consensus  ********** ********** ********** ********** **********

                            2151                                               2200
     msa235280.2{195_COH1}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
     msa235280.2{195_M732}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
     msa235280.2{195_M781}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
     msa235280.2{195_H36B}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
msa235280.2{195_JM9130013}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
   msa235280.2{195_18RS21}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
     msa235280.2{195_2603}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
     msa235280.2{195_A909}  TAGGAACCCC TGTTATTATT CAAGGTAAAG ACTTGACTAA TCGAACAAAA
                 Consensus  ********** ********** ********** ********** **********

                            2201                                               2250
     msa235280.2{195_COH1}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
     msa235280.2{195_M732}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
     msa235280.2{195_M781}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
     msa235280.2{195_H36B}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
msa235280.2{195_JM9130013}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
   msa235280.2{195_18RS21}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
     msa235280.2{195_2603}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
     msa235280.2{195_A909}  CCATTAATGA GTGGACGTAG AGTACTTTAT GCCGGTAAAC AATATGAGTT
                 Consensus  ********** ********** ********** ********** **********

                            2251                                               2300
     msa235280.2{195_COH1}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
     msa235280.2{195_M732}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
     msa235280.2{195_M781}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
     msa235280.2{195_H36B}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
msa235280.2{195_JM9130013}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
   msa235280.2{195_18RS21}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
     msa235280.2{195_2603}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
     msa235280.2{195_A909}  CCGGGCTAAA TTACCACTTA GTCGTTTTAA CACTTGGATT AGGGTTGAAG
                 Consensus  ********** ********** ********** ********** **********

                            2301                                               2350
     msa235280.2{195_COH1}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
     msa235280.2{195_M732}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
     msa235280.2{195_M781}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
     msa235280.2{195_H36B}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
msa235280.2{195_JM9130013}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
   msa235280.2{195_18RS21}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
     msa235280.2{195_2603}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
     msa235280.2{195_A909}  TGGTAACAGA AGCAGGAGAG AAAGCAAGTA TTGTTCGTCG CATGTTCTTT
                 Consensus  ********** ********** ********** ********** **********

                            2351                                               2400
     msa235280.2{195_COH1}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
     msa235280.2{195_M732}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
     msa235280.2{195_M781}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
     msa235280.2{195_H36B}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
msa235280.2{195_JM9130013}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
   msa235280.2{195_18RS21}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
     msa235280.2{195_2603}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
     msa235280.2{195_A909}  GACCAATCAG TTCCAGAGCT TAACACAGCA GTTGCTAAAC GTGATTTGAC
                 Consensus  ********** ********** ********** ********** **********

                            2401                                               2450
     msa235280.2{195_COH1}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
     msa235280.2{195_M732}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
     msa235280.2{195_M781}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
     msa235280.2{195_H36B}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
msa235280.2{195_JM9130013}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
   msa235280.2{195_18RS21}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
     msa235280.2{195_2603}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
```

Table 51: Comparative Sequences relating to SAG0677

```
     msa235280.2{195_A909}  TTCTGATACT GCTCTTATCC ACATCGTTGC CAAAGATGAC TCTCTAAAAC
                 Consensus  ********** ********** ********** ********** **********

                            2451                                              2500
     msa235280.2{195_COH1}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
     msa235280.2{195_M732}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
     msa235280.2{195_M781}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
     msa235280.2{195_H36B}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
msa235280.2{195_JM9130013}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
   msa235280.2{195_18RS21}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
     msa235280.2{195_2603}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
     msa235280.2{195_A909}  TAAAATTATA TCAAGATGAT TCATTACTTG AATCTGTTGA TAAAACCGGT
                 Consensus  ********** ********** ********** ********** **********

                            2501                                              2550
     msa235280.2{195_COH1}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
     msa235280.2{195_M732}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
     msa235280.2{195_M781}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
     msa235280.2{195_H36B}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
msa235280.2{195_JM9130013}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
   msa235280.2{195_18RS21}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
     msa235280.2{195_2603}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
     msa235280.2{195_A909}  CTTTATAGTT TTAGAAATGG TGTAGAAATC ACTAAAGATA TGACAGTACC
                 Consensus  ********** ********** ********** ********** **********

                            2551                                              2600
     msa235280.2{195_COH1}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
     msa235280.2{195_M732}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
     msa235280.2{195_M781}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
     msa235280.2{195_H36B}  ACTAGAATTT GGAGATAATA TTAcTAAGTT ATCTGCTGTT GACTTATCAA
msa235280.2{195_JM9130013}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
   msa235280.2{195_18RS21}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
     msa235280.2{195_2603}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
     msa235280.2{195_A909}  ACTAGAATTT GGAGATAATA TTAtTAAGTT ATCTGCTGTT GACTTATCAA
                 Consensus  ********** ********** ***_****** ********** **********

                            2601                                              2650
     msa235280.2{195_COH1}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
     msa235280.2{195_M732}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
     msa235280.2{195_M781}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
     msa235280.2{195_H36B}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
msa235280.2{195_JM9130013}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
   msa235280.2{195_18RS21}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
     msa235280.2{195_2603}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
     msa235280.2{195_A909}  ATTATCGTCG TAATGAGACC CTTCATATCT ATAGAAACCG TTTTGATGTT
                 Consensus  ********** ********** ********** ********** **********

                            2651                                              2700
     msa235280.2{195_COH1}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
     msa235280.2{195_M732}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
     msa235280.2{195_M781}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
     msa235280.2{195_H36B}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
msa235280.2{195_JM9130013}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
   msa235280.2{195_18RS21}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
     msa235280.2{195_2603}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
     msa235280.2{195_A909}  AAAGCAAGCC AAATGACAGC TGACAAAGGA GCTAAAGTAA CTGTGGATAT
                 Consensus  ********** ********** ********** ********** **********

                            2701                                              2750
     msa235280.2{195_COH1}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
     msa235280.2{195_M732}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
     msa235280.2{195_M781}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
     msa235280.2{195_H36B}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
msa235280.2{195_JM9130013}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
   msa235280.2{195_18RS21}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
     msa235280.2{195_2603}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
     msa235280.2{195_A909}  GTTGATGAAG CACTTAGTTG TTCCAGAAAT GGCAGGAGCT TATACATTAA
                 Consensus  ********** ********** ********** ********** **********

                            2751                                              2800
     msa235280.2{195_COH1}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
     msa235280.2{195_M732}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
     msa235280.2{195_M781}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
     msa235280.2{195_H36B}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
msa235280.2{195_JM9130013}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
   msa235280.2{195_18RS21}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
     msa235280.2{195_2603}  CAATCGACGA AGcTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
     msa235280.2{195_A909}  CAATCGACGA AGaTCCAAAC ACAAATGAAT CAGGAATGTT AACAAACGCT
                 Consensus  ********** **_******* ********** ********** **********

                            2801                                              2850
     msa235280.2{195_COH1}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
     msa235280.2{195_M732}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
```

Table 51: Comparative Sequences relating to SAG0677

```
     msa235280.2{195_M781}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
     msa235280.2{195_H36B}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
msa235280.2{195_JM9130013}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
   msa235280.2{195_18RS21}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
     msa235280.2{195_2603}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
     msa235280.2{195_A909}  AAAGTATCGA TTCATTATGT AAATGGTGGT GTTGATAAAG TTGATGTTCC
                 Consensus  ********** ********** ********** ********** **********

                            2851                                              2900
     msa235280.2{195_COH1}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
     msa235280.2{195_M732}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
     msa235280.2{195_M781}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
     msa235280.2{195_H36B}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
msa235280.2{195_JM9130013}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
   msa235280.2{195_18RS21}  GATTAAAGTA GTTGACTTAG AAGCTATT.. .......... ..........
     msa235280.2{195_2603}  GATTAAAGTA GTTGACTTAG AAGCTATT.. .......... ..........
     msa235280.2{195_A909}  GATTAAAGTA GTTGACTTAG AAGCTATTcg taaagctgaa gaagcacata
                 Consensus  ********** ********** ********-- ---------- ----------

                            2901                                              2950
     msa235280.2{195_COH1}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
     msa235280.2{195_M732}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
     msa235280.2{195_M781}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
     msa235280.2{195_H36B}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAcGAAGCA
msa235280.2{195_JM9130013}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
   msa235280.2{195_18RS21}  .......... .......... .......... ..CGTAAAGC TGAaGAAGCA
     msa235280.2{195_2603}  .......... ....cgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
     msa235280.2{195_A909}  aagctgacga agcacgtaaa gctgaagaag caCGTAAAGC TGAaGAAGCA
                 Consensus  ---------- ---------- ---------- --******** ***-******

                            2951                                              3000
     msa235280.2{195_COH1}  CaTAAAGCTG AAGAAGtAcg taaagctgaa gaagcacata aagtcgaaga
     msa235280.2{195_M732}  CaTAAAGCTG AAGAAGtAcg taaagctgaa gaagcacata aagtcgaaga
     msa235280.2{195_M781}  CaTAAAGCTG AAGAAGtAcg taaagctgaa gaagcacata aagtcgaaga
     msa235280.2{195_H36B}  CaTAAAGCTG AAGAAGtAcg taaagctgaa gaagcacata aagtcgaaga
msa235280.2{195_JM9130013}  CaTAAAGCTG AAGAAGtAcg taaagctgaa gaagcacata aagtcgaaga
   msa235280.2{195_18RS21}  CgTAAAGCTG AAGAAGcA.. .......... .......... ..........
     msa235280.2{195_2603}  CgTAAAGCTG AAGAAGcA.. .......... .......... ..........
     msa235280.2{195_A909}  CgTAAAGCTG AAGAAGcA.. .......... .......... ..........
                 Consensus  *-******** ******-*-- ---------- ---------- ----------

                            3001                                              3050
     msa235280.2{195_COH1}  agca.CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
     msa235280.2{195_M732}  agca.CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
     msa235280.2{195_M781}  agcacCGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
     msa235280.2{195_H36B}  agca.CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
msa235280.2{195_JM9130013}  agcacCGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
   msa235280.2{195_18RS21}  .....CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
     msa235280.2{195_2603}  .....CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
     msa235280.2{195_A909}  .....CGTAA AGCTGAAGAG GGACATAAAA CCCAAGAAGC ACCTATAGTT
                 Consensus  -----***** ********** ********** ********** **********

                            3051                                              3100
     msa235280.2{195_COH1}  GAAGAAGGCT ACAAaGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
     msa235280.2{195_M732}  GAAGAAGGCT ACAAaGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
     msa235280.2{195_M781}  GAAGAAGGCT ACAAaGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
     msa235280.2{195_H36B}  GAAGAAGGCT ACAAgGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
msa235280.2{195_JM9130013}  GAAGAAGGCT ACAAgGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
   msa235280.2{195_18RS21}  GAAGAAGGCT ACAAgGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
     msa235280.2{195_2603}  GAAGAAGGCT ACAAgGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
     msa235280.2{195_A909}  GAAGAAGGCT ACAAgGTTAA TAACGTTCAT CAAACTGATA CTACAGTTAA
                 Consensus  ********** ****-***** ********** ********** **********

                            3101                                              3150
     msa235280.2{195_COH1}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
     msa235280.2{195_M732}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
     msa235280.2{195_M781}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
     msa235280.2{195_H36B}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
msa235280.2{195_JM9130013}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
   msa235280.2{195_18RS21}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
     msa235280.2{195_2603}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
     msa235280.2{195_A909}  AGCGTCTGAT TTACCAAAGA CTAAGACAGT TTCCGCAGTT CATATGGCTA
                 Consensus  ********** ********** ********** ********** **********

                            3151                                              3200
     msa235280.2{195_COH1}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt ~~~~~~~~~~
     msa235280.2{195_M732}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TGAAAA~~~~
     msa235280.2{195_M781}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TG~~~~~~~~
     msa235280.2{195_H36B}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATG~ ~~~~~~~~~~
msa235280.2{195_JM9130013}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TG~~~~~~~~
   msa235280.2{195_18RS21}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TGAA~~~~~~
     msa235280.2{195_2603}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TGAAAAACAA
     msa235280.2{195_A909}  GAACAGACAA TAAACAGATA ACTTCACATC AGACACATGt TGAAAAACAA
```

Table 51: Comparative Sequences relating to SAG0677

```
                Consensus  ********** ********** ********** ********** **********

                           3201                                              3250
  msa235280.2{195_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa235280.2{195_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa235280.2{195_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_2603}    ATTAAAAATA cattgccatc cactggtgac agcaaacgtg gttattatat
  msa235280.2{195_A909}    ATTAAAAATA ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ********** ********** ********** **********

                           3251                                              3300
  msa235280.2{195_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa235280.2{195_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa235280.2{195_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa235280.2{195_2603}    cactggaatg gctatcgtta tgctgagtgt attatttagt ttagctaaaa
  msa235280.2{195_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ********** ********** ********** **********

                           3301       3317
  msa235280.2{195_COH1}    ~~~~~~~~~~ ~~~~~~~
  msa235280.2{195_M732}    ~~~~~~~~~~ ~~~~~~~
  msa235280.2{195_M781}    ~~~~~~~~~~ ~~~~~~~
  msa235280.2{195_H36B}    ~~~~~~~~~~ ~~~~~~~
msa235280.2{195_JM9130013} ~~~~~~~~~~ ~~~~~~~
 msa235280.2{195_18RS21}   ~~~~~~~~~~ ~~~~~~~
  msa235280.2{195_2603}    agtttaaaag caaatat
  msa235280.2{195_A909}    ~~~~~~~~~~ ~~~~~~~
                Consensus  ********** *******
```

SEQ ID NO. 5110
STRAIN 2603 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDGPILASKV
NGKILQVESDGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAV
DYLSNTTFEQLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDSLSVRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELD
MFFKQSQDPASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYYIYKDAINLKFKLTSG
ASLKVVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
VVKGSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTP
VIIQGKDLTNRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
VEITKDMTVPLEFGDNIIKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDM
LMKHLVVPEMAGAYTLTIDEAPNTNESGMLTNAKVSIHYVNGGVDKVDVPIKVVDLEAIR
KAEEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVNNVHQTDTTVKASDLPKTKTVS
AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYYITGMAIVMLSVLFSLAKKFKSK
Y

SEQ ID NO. 5111
STRAIN A909 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPPPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEALKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAV
DYLSNTTFEQLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDSLSVRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELD
MFFKQSQDPASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYYIYKDAINLKFKLTSG
ASLKVVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
VGKGSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTP
VIIQGKDLTNRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
VEITKDMTVPLEFGDNIIKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDM
LMKHLVVPEMAGAYTLTIDEDPNTNESGMLTNAKVSIHYVNGGVDKVDVPIKVVDLEAIR
KAEEAHKADEARKAEEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVNNVHQTDTTV
KASDLPKTKTVSAVHMARTDNKQITSHQTHVEKQIKN

SEQ ID NO. 5112
STRAIN H36B frame: 2
GVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVYLQSVKYVGG
GNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTKPSKPKDSLS
TPPGFPDLNTPPDEALKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES

Table 51: Comparative Sequences relating to SAG0677

DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAVDYLSNTTFE
QLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGIELPNDVRHI
DSLSVRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSSEIMTTFK
DGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELDMFFKQSQDP
ASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYYIYKDAINLKFKLTSGASLKVVYKG
QEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKEVGKGSELPL
TKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDMLLTMQKDSAY
YETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSEHKYPSVFLL
TPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTPVIIQGKDLT
NRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRRMFFDQSVPE
LNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNGVEITKDMTV
PLEFGDNITKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDMLMKHLVVPE
MAGAYTLTIDEAPNTNESGMLTNAKVSIHYVNGGVDKVDVPIKVVDLEAIRKAEEAHKAD
EARKAEEARKADEAHKAEEVRKAEEAHKVEEARKAEEGHKTQEAPIVEEGYKVNNVHQTD
TTVKASDLPKTKTVSAVHMARTDNKQITSHQTH

SEQ ID NO. 5113
STRAIN 18RS21 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAV
DYLSNTTFEQLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDSLSVRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELD
MFFKQSQDPASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYYIYKDAINLKFKLTSG
ASLKVVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
VVKGSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTP
VIIQGKDLTNRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
VEITKDMTVPLEFGDNIIKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDM
LMKHLVVPEMAGAYTLTIDEAPNTNESGMLTNAKVSIHYVNGGVDKVDVPIKVVDLEAIR
KAEEARKAEEARKAEEGHKTQEAPIVEEGYKVNNVHQTDTTVKASDLPKTKTVSAVHMAR
TDNKQITSHQTHVE

SEQ ID NO. 5114
STRAIN M732 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNITSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYYHNRLFCRYKICQYHSG
.LFEQYYF.AISYW.NSRLPCHCIFKLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQQNLPIKIQPDKSSSRVYY..H.L
KFRNHDHFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTTYCKNWNS.IR
YVFQTISRPSFNY.KNIPYPKWCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIKC.KFDYGDG.CK.ESSTTSFKS.II.K.AYEGYA
TYYAKRFSVLRNK.QSSPSN.SHCRY.T.F.CC.RSECSY.KYDDETVCSCWTTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCQR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLYINNRRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC.K

SEQ ID NO. 5115
STRAIN COH1 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK
PSKPKDSLSTPPGFPDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNITSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYYHNRLFCRYKICQYHSG
.LFEQYYF.AISYW.NSRLPCHCIFKLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQQNLPIKIQPDKSSSRVYY..H.L
KFRNHDHFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTTYCKNWNS.IR
YVFQTISRPSFNY.KNIPYPKWCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIKC.KFDYGDG.CK.ESSTTSFKS.II.K.AYEGYA
TYYAKRFSVLRNK.QSSPSN.SHCRY.T.F.CC.RSECSY.KYDDETVCSCWTTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCQR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLYINNRRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

SEQ ID NO. 5116
STRAIN M781 frame: 1
LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK

Table 51: Comparative Sequences relating to SAG0677

```
PSKPKDSLSTPPGFPDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNITSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYYHNRLFCRYKICQYHSG
.LFEQYYF.AISYW.NSRLPCHCIFKLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQQNLPIKIQPDKSSSRVYY..H.L
KFRNHDHFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTTYCKNWNS.IR
YVFQTISRPSFNY.KNIPYPKWCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIKC.KFDYGDG.CK.ESSTTSFKS.II.K.AYEGYA
TYYAKRFSVLRNK.QSSPSN.SHCRY.T.F.CC.RSECSY.KYDDETVCSCWTTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCQR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLYINNRRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRSTVKLKRDIKPKKHL.LKKA
TKLITFIKLILQLKRLIYQRLRQFPQFIWLEQTINR.LHIRHML
```

SEQ ID NO. 5117

```
STRAIN JM9130013 frame: 2
GVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVYLQSVKYVGG
GNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTKPSKPKDSLS
TPPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES
DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAVDYLSNTTFE
QLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGIELPNDVRHI
DSLSVRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSSEIMTTFK
DGKMPELVEQKDVSLDINDMDMSKFKTIRLGRKDSEFKGQLIAKTGTVELDMFFKQSQDP
ASIIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYYIYKDAINLKFKLTSGASLKVVYKG
QEDPYSHQKEDMTKXGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKEVGKGSELPL
TKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDMLLTMQKDSAY
YETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSEHKYPSVFLL
TPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMLGTPVIIQGKDLT
NRTKPLMSGRRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRRMFFDQSVPE
LNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNGVEITKDMTV
PLEFGDNIIKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVDMLMKHLVVPE
MAGAYTLTIDEAPNTNESGMLTNAKVSIHYVNGGVDKVDVPIKVVDLEAIRKAEEAHKAD
EARKAEEARKAEEAHKAEEVRKAEEAHKVEEAP.S.RGT.NPRSTYS.RRLQG..RSSN.
YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC
```

```
PRETTY of: /biotmp/msa235427.2{*}   December 10, 2002 05:18  ..

                             1                                                  50
      msa235427.2{195_H36B}  ~~~~~~~~~G VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
  msa235427.2{195_JM9130013}  ~~~~~~~~~G VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
    msa235427.2{195_18RS21}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
      msa235427.2{195_2603}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
      msa235427.2{195_A909}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
      msa235427.2{195_COH1}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
      msa235427.2{195_M732}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
      msa235427.2{195_M781}  LNNKGVGGDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
                  Consensus  ********** ********** ********** ********** **********

                             51                                                100
      msa235427.2{195_H36B}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
  msa235427.2{195_JM9130013}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
    msa235427.2{195_18RS21}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
      msa235427.2{195_2603}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
      msa235427.2{195_A909}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
      msa235427.2{195_COH1}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
      msa235427.2{195_M732}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
      msa235427.2{195_M781}  DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPKLDRPPGI
                  Consensus  ********** ********** ********** ********** **********

                             101                                               150
      msa235427.2{195_H36B}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
  msa235427.2{195_JM9130013}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
    msa235427.2{195_18RS21}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
      msa235427.2{195_2603}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
      msa235427.2{195_A909}  DLPpPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
      msa235427.2{195_COH1}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
      msa235427.2{195_M732}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
      msa235427.2{195_M781}  DLPaPTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
                  Consensus  ***-****** ********** ********** ********** ****-*---*

                             151                                               200
      msa235427.2{195_H36B}  daiedksgai kyakslqlsf vddPilaskv ngkilqvesd gklviprnal
  msa235427.2{195_JM9130013}  daiedksgai kyakslqlsf vddPilaskv ngkilqvesd gklviprnal
    msa235427.2{195_18RS21}  daiedksgai kyakslqlsf vddPilaskv ngkilqvesd gklviprnal
      msa235427.2{195_2603}  daiedksgai kyakslqlsf vdgPilaskv ngkilqvesd gklviprnal
      msa235427.2{195_A909}  daiedksgai kyakslqlsf vddPilaskv ngkilqvesd gklviprnal
      msa235427.2{195_COH1}  rry.r.irsn .ic.vsst.l c..Pyfs.qs kwqnitsri. wqishs.kcf
      msa235427.2{195_M732}  rry.r.irsn .ic.vsst.l c..Pyfs.qs kwqnitsri. wqishs.kcf
      msa235427.2{195_M781}  rry.r.irsn .ic.vsst.l c..Pyfs.qs kwqnitsri. wqishs.kcf
                  Consensus  ---------- ---------- ---*------ ---------- ----------
```

Table 51: Comparative Sequences relating to SAG0677

```
                            201                                                250
     msa235427.2{195_H36B}  sanqfddtsl kiyrnnnrnk eitittdyFa dtKyvnitav dylsnttFeq
msa235427.2{195_JM9130013}  sanqfddtsl kiyrnnnrnk eitittdyFa dtKyvnitav dylsnttFeq
   msa235427.2{195_18RS21}  sanqfddtsl kiyrnnnrnk eitittdyFa dtKyvnitav dylsnttFeq
     msa235427.2{195_2603}  sanqfddtsl kiyrnnnrnk eitittdyFa dtKyvnitav dylsnttFeq
     msa235427.2{195_A909}  sanqfddtsl kiyrnnnrnk eitittdyFa dtKyvnitav dylsnttFeq
     msa235427.2{195_COH1}  vs.si..h.s .nls...sq. rnyyhnrlFc ryKicqyhsg .lfeqyyF.a
     msa235427.2{195_M732}  vs.si..h.s .nls...sq. rnyyhnrlFc ryKicqyhsg .lfeqyyF.a
     msa235427.2{195_M781}  vs.si..h.s .nls...sq. rnyyhnrlFc ryKicqyhsg .lfeqyyF.a
                 Consensus  ---------- ---------- --------*- --*------- -------*--

                            251                                                300
     msa235427.2{195_H36B}  latgetvdyh aivfssfaai kdkGgkiyvn dklqetsria lkdksvkigi
msa235427.2{195_JM9130013}  latgetvdyh aivfssfaai kdkGgkiyvn dklqetsria lkdksvkigi
   msa235427.2{195_18RS21}  latgetvdyh aivfssfaai kdkGgkiyvn dklqetsria lkdksvkigi
     msa235427.2{195_2603}  latgetvdyh aivfssfaai kdkGgkiyvn dklqetsria lkdksvkigi
     msa235427.2{195_A909}  latgetvdyh aivfssfaai kdkGgkiyvn dklqetsria lkdksvkigi
     msa235427.2{195_COH1}  isyw.nsrlp chcifklccy .rqGw.dlc. r.iarnfsys a.r.ic.dwy
     msa235427.2{195_M732}  isyw.nsrlp chcifklccy .rqGw.dlc. r.iarnfsys a.r.ic.dwy
     msa235427.2{195_M781}  isyw.nsrlp chcifklccy .rqGw.dlc. r.iarnfsys a.r.ic.dwy
                 Consensus  ---------- ---------- ---*------ ---------- ----------

                            301                                                350
     msa235427.2{195_H36B}  elpndvrhid slsvrrlnev ktvdniLknd eqdinlskty qlKynPtnrr
msa235427.2{195_JM9130013}  elpndvrhid slsvrrlnev ktvdniLknd eqdinlskty qlKynPtnrr
   msa235427.2{195_18RS21}  elpndvrhid slsvrrlnev ktvdniLknd eqdinlskty qlKynPtnrr
     msa235427.2{195_2603}  elpndvrhid slsvrrlnev ktvdniLknd eqdinlskty qlKynPtnrr
     msa235427.2{195_A909}  elpndvrhid slsvrrlnev ktvdniLknd eqdinlskty qlKynPtnrr
     msa235427.2{195_COH1}  .itk.cqty. .ficssfe.g .nc..yLek. .trh.sqqnl piKiqPdkss
     msa235427.2{195_M732}  .itk.cqty. .ficssfe.g .nc..yLek. .trh.sqqnl piKiqPdkss
     msa235427.2{195_M781}  .itk.cqty. .ficssfe.g .nc..yLek. .trh.sqqnl piKiqPdkss
                 Consensus  ---------- ---------- ------*--- ---------- --*--*----

                            351                                                400
     msa235427.2{195_H36B}  leftinnins sseimttFkd gKmpelveqK dvsldindmd mskfktirlg
msa235427.2{195_JM9130013}  leftinnins sseimttFkd gKmpelveqK dvsldindmd mskfktirlg
   msa235427.2{195_18RS21}  leftinnins sseimttFkd gKmpelveqK dvsldindmd mskfktirlg
     msa235427.2{195_2603}  leftinnins sseimttFkd gKmpelveqK dvsldindmd mskfktirlg
     msa235427.2{195_A909}  leftinnins sseimttFkd gKmpelveqK dvsldindmd mskfktirlg
     msa235427.2{195_COH1}  srvyy..h.l kfrnhdhFqr wKdarig.tK rcffgykryg he.v.nystw
     msa235427.2{195_M732}  srvyy..h.l kfrnhdhFqr wKdarig.tK rcffgykryg he.v.nystw
     msa235427.2{195_M781}  srvyy..h.l kfrnhdhFqr wKdarig.tK rcffgykryg he.v.nystw
                 Consensus  ---------- -------*-- -*-------* ---------- ----------

                            401                                                450
     msa235427.2{195_H36B}  rKdsefkGql iaKtgtveld mfFkqsqdPa siikKiyliq ngvpnelkKf
msa235427.2{195_JM9130013}  rKdsefkGql iaKtgtveld mfFkqsqdPa siikKiyliq ngvpnelkKf
   msa235427.2{195_18RS21}  rKdsefkGql iaKtgtveld mfFkqsqdPa siikKiyliq ngvpnelkKf
     msa235427.2{195_2603}  rKdsefkGql iaKtgtveld mfFkqsqdPa siikKiyliq ngvpnelkKf
     msa235427.2{195_A909}  rKdsefkGql iaKtgtveld mfFkqsqdPa siikKiyliq ngvpnelkKf
     msa235427.2{195_COH1}  tKgf.i.Gtt ycKnwns.ir yvFqtisrPs fny.Knipyp kwcsk.ieKi
     msa235427.2{195_M732}  tKgf.i.Gtt ycKnwns.ir yvFqtisrPs fny.Knipyp kwcsk.ieKi
     msa235427.2{195_M781}  tKgf.i.Gtt ycKnwns.ir yvFqtisrPs fny.Knipyp kwcsk.ieKi
                 Consensus  -*-----*-- --*------- --*-----*- ----*----- --------*-

                            451                                                500
     msa235427.2{195_H36B}  dssFgltesq idgyyiykda inlkfkltsg aslkvvykgq edpyshqked
msa235427.2{195_JM9130013}  dssFgltesq idgyyiykda inlkfkltsg aslkvvykgq edpyshqked
   msa235427.2{195_18RS21}  dssFgltesq idgyyiykda inlkfkltsg aslkvvykgq edpyshqked
     msa235427.2{195_2603}  dssFgltesq idgyyiykda inlkfkltsg aslkvvykgq edpyshqked
     msa235427.2{195_A909}  dssFgltesq idgyyiykda inlkfkltsg aslkvvykgq edpyshqked
     msa235427.2{195_COH1}  .l.Fwfn.ks drwilyl.rc n.p.i.inqw cks.scl.ra rrsi.sserr
     msa235427.2{195_M732}  .l.Fwfn.ks drwilyl.rc n.p.i.inqw cks.scl.ra rrsi.sserr
     msa235427.2{195_M781}  .l.Fwfn.ks drwilyl.rc n.p.i.inqw cks.scl.ra rrsi.sserr
                 Consensus  ---*------ ---------- ---------- ---------- ----------

                            501                                                550
     msa235427.2{195_H36B}  mtkkgeqlsh stqanentaK vtfanidwsh yskvtvngKe vgkgselplt
msa235427.2{195_JM9130013}  mtkxgeqlsh stqanentaK vtfanidwsh yskvtvngKe vgkgselplt
   msa235427.2{195_18RS21}  mtkkgeqlsh stqanentaK vtfanidwsh yskvtvngKe vvkgselplt
     msa235427.2{195_2603}  mtkkgeqlsh stqanentaK vtfanidwsh yskvtvngKe vvkgselplt
     msa235427.2{195_A909}  mtkkgeqlsh stqanentaK vtfanidwsh yskvtvngKe vgkgselplt
     msa235427.2{195_COH1}  yd.kr.taqs fnssq.kysK snlc.y.lvt l..gycewKr sw.r..vtfn
     msa235427.2{195_M732}  yd.kr.taqs fnssq.kysK snlc.y.lvt l..gycewKr sw.r..vtfn
     msa235427.2{195_M781}  yd.kr.taqs fnssq.kysK snlc.y.lvt l..gycewKr sw.r..vtfn
                 Consensus  ---------- ---------* ---------- --------*- ----------

                            551                                                600
     msa235427.2{195_H36B}  kgwttfvlhk tenslnvksl imetGsvskk vqqlplsprl sknkhmrdml
msa235427.2{195_JM9130013}  kgwttfvlhk tenslnvksl imetGsvskk vqqlplsprl sknkhmrdml
   msa235427.2{195_18RS21}  kgwttfvlhk tenslnvksl imetGsvskk vqqlplsprl sknkhmrdml
     msa235427.2{195_2603}  kgwttfvlhk tenslnvksl imetGsvskk vqqlplsprl sknkhmrdml
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Table 51: Comparative Sequences relating to SAG0677

```
     msa235427.2{195_A909}  kgwttfvlhk tenslnvksl imetGsvskk vqqlplsprl sknkhmrdml
     msa235427.2{195_COH1}  .rmdnicit. nrkfikc.kf dygdG.ck.e ssttsfks.i i.k.ayegy.
     msa235427.2{195_M732}  .rmdnicit. nrkfikc.kf dygdG.ck.e ssttsfks.i i.k.ayegy.
     msa235427.2{195_M781}  .rmdnicit. nrkfikc.kf dygdG.ck.e ssttsfks.i i.k.ayegy.
                 Consensus  ---------- ---------- ----*----- ---------- ----------

                            601                                                650
     msa235427.2{195_H36B}  lTmqkdsayy etsdslvlri Nltadtklnf navkgaSalt enmmmrqfav
msa235427.2{195_JM9130013}  lTmqkdsayy etsdslvlri Nltadtklnf navkgaSalt enmmmrqfav
   msa235427.2{195_18RS21}  lTmqkdsayy etsdslvlri Nltadtklnf navkgaSalt enmmmrqfav
     msa235427.2{195_2603}  lTmqkdsayy etsdslvlri Nltadtklnf navkgaSalt enmmmrqfav
     msa235427.2{195_A909}  lTmqkdsayy etsdslvlri Nltadtklnf navkgaSalt enmmmrqfav
     msa235427.2{195_COH1}  aTyyakrfsv lrnk.qssps N.shcry.t. f.cc.rSecs y.kyddetvc
     msa235427.2{195_M732}  aTyyakrfsv lrnk.qssps N.shcry.t. f.cc.rSecs y.kyddetvc
     msa235427.2{195_M781}  aTyyakrfsv lrnk.qssps N.shcry.t. f.cc.rSecs y.kyddetvc
                 Consensus  -*-------- ---------- *--------- ------*--- ----------

                            651                                                700
     msa235427.2{195_H36B}  agpqddpvse hkypsvfllt palLetasea tlngkeitaS giighikdGd
msa235427.2{195_JM9130013}  agpqddpvse hkypsvfllt palLetasea tlngkeitaS giighikdGd
   msa235427.2{195_18RS21}  agpqddpvse hkypsvfllt palLetasea tlngkeitaS giighikdGd
     msa235427.2{195_2603}  agpqddpvse hkypsvfllt palLetasea tlngkeitaS giighikdGd
     msa235427.2{195_A909}  agpqddpvse hkypsvfllt palLetasea tlngkeitaS giighikdGd
     msa235427.2{195_COH1}  scwttr.sc. .t.ipisisl nscLignc.. gnskw.gnhS iwyyrshqGw
     msa235427.2{195_M732}  scwttr.sc. .t.ipisisl nscLignc.. gnskw.gnhS iwyyrshqGw
     msa235427.2{195_M781}  scwttr.sc. .t.ipisisl nscLignc.. gnskw.gnhS iwyyrshqGw
                 Consensus  ---------- ---------- ---*------ ---------* --------*-

                            701                                                750
     msa235427.2{195_H36B}  ksKhvevkmv nEngdmlgtp viiqgkdltn rtkplmsgrr vlyagkqyef
msa235427.2{195_JM9130013}  ksKhvevkmv nEngdmlgtp viiqgkdltn rtkplmsgrr vlyagkqyef
   msa235427.2{195_18RS21}  ksKhvevkmv nEngdmlgtp viiqgkdltn rtkplmsgrr vlyagkqyef
     msa235427.2{195_2603}  ksKhvevkmv nEngdmlgtp viiqgkdltn rtkplmsgrr vlyagkqyef
     msa235427.2{195_A909}  ksKhvevkmv nEngdmlgtp viiqgkdltn rtkplmsgrr vlyagkqyef
     msa235427.2{195_COH1}  ..Kqac.sqn gE.kwrharn pcyysr.rld .snktinewt .stlcr.ti.
     msa235427.2{195_M732}  ..Kqac.sqn gE.kwrharn pcyysr.rld .snktinewt .stlcr.ti.
     msa235427.2{195_M781}  ..Kqac.sqn gE.kwrharn pcyysr.rld .snktinewt .stlcr.ti.
                 Consensus  --*------- -*-------- ---------- ---------- ----------

                            751                                                800
     msa235427.2{195_H36B}  raklplsrfn twirvevvte agekaSivrr mffdqsvpel ntavakrdlt
msa235427.2{195_JM9130013}  raklplsrfn twirvevvte agekaSivrr mffdqsvpel ntavakrdlt
   msa235427.2{195_18RS21}  raklplsrfn twirvevvte agekaSivrr mffdqsvpel ntavakrdlt
     msa235427.2{195_2603}  raklplsrfn twirvevvte agekaSivrr mffdqsvpel ntavakrdlt
     msa235427.2{195_A909}  raklplsrfn twirvevvte agekaSivrr mffdqsvpel ntavakrdlt
     msa235427.2{195_COH1}  vpg.itt.sf .hld.g.sgn rsrreSkycs shvl.pissr a.hssc.t.f
     msa235427.2{195_M732}  vpg.itt.sf .hld.g.sgn rsrreSkycs shvl.pissr a.hssc.t.f
     msa235427.2{195_M781}  vpg.itt.sf .hld.g.sgn rsrreSkycs shvl.pissr a.hssc.t.f
                 Consensus  ---------- ---------- -----*---- ---------- ----------

                            801                                                850
     msa235427.2{195_H36B}  sdtalihiva kddsLklkly qddsllesvd ktglysfrng veitkdmtvp
msa235427.2{195_JM9130013}  sdtalihiva kddsLklkly qddsllesvd ktglysfrng veitkdmtvp
   msa235427.2{195_18RS21}  sdtalihiva kddsLklkly qddsllesvd ktglysfrng veitkdmtvp
     msa235427.2{195_2603}  sdtalihiva kddsLklkly qddsllesvd ktglysfrng veitkdmtvp
     msa235427.2{195_A909}  sdtalihiva kddsLklkly qddsllesvd ktglysfrng veitkdmtvp
     msa235427.2{195_COH1}  df.ycsyphr cqr.Lsktki isr.fit.ic ..nrsl.f.k wcrnh.ryds
     msa235427.2{195_M732}  df.ycsyphr cqr.Lsktki isr.fit.ic ..nrsl.f.k wcrnh.ryds
     msa235427.2{195_M781}  df.ycsyphr cqr.Lsktki isr.fit.ic ..nrsl.f.k wcrnh.ryds
                 Consensus  ---------- ----*----- ---------- ---------- ----------

                            851                                                900
     msa235427.2{195_H36B}  lefgdnitkl savdlsnyrr netlhiYrnr fdvkaSqmta dkgakvtvdm
msa235427.2{195_JM9130013}  lefgdniikl savdlsnyrr netlhiYrnr fdvkaSqmta dkgakvtvdm
   msa235427.2{195_18RS21}  lefgdniikl savdlsnyrr netlhiYrnr fdvkaSqmta dkgakvtvdm
     msa235427.2{195_2603}  lefgdniikl savdlsnyrr netlhiYrnr fdvkaSqmta dkgakvtvdm
     msa235427.2{195_A909}  lefgdniikl savdlsnyrr netlhiYrnr fdvkaSqmta dkgakvtvdm
     msa235427.2{195_COH1}  ttriwr.yy. vicc.likls s..dpsYl.k pf.c.Skpnd s.qrs.sncg
     msa235427.2{195_M732}  ttriwr.yy. vicc.likls s..dpsYl.k pf.c.Skpnd s.qrs.sncg
     msa235427.2{195_M781}  ttriwr.yy. vicc.likls s..dpsYl.k pf.c.Skpnd s.qrs.sncg
                 Consensus  ---------- ---------- ------*--- -----*---- ----------

                            901                                                950
     msa235427.2{195_H36B}  lmkhlvvpem aGaytltide apntnesgml tNakvSIhyv nggvdkvdvp
msa235427.2{195_JM9130013}  lmkhlvvpem aGaytltide apntnesgml tNakvSIhyv nggvdkvdvp
   msa235427.2{195_18RS21}  lmkhlvvpem aGaytltide apntnesgml tNakvSIhyv nggvdkvdvp
     msa235427.2{195_2603}  lmkhlvvpem aGaytltide apntnesgml tNakvSIhyv nggvdkvdvp
     msa235427.2{195_A909}  lmkhlvvpem aGaytltide dpntnesgml tNakvSIhyv nggvdkvdvp
     msa235427.2{195_COH1}  yvdealscsr nGrslyinnr rsskhk.irn vNkr.SIdsl ckwwc..s.c
     msa235427.2{195_M732}  yvdealscsr nGrslyinnr rsskhk.irn vNkr.SIdsl ckwwc..s.c
     msa235427.2{195_M781}  yvdealscsr nGrslyinnr rsskhk.irn vNkr.SIdsl ckwwc..s.c
                 Consensus  ---------- -*-------- ---------- -*---**--- ----------
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Table 51: Comparative Sequences relating to SAG0677

```
                            951                                               1000
     msa235427.2{195_H36B}  ikvvdleair kaeeahkade arkaeearka deahkaeevr kaeeahkvee
msa235427.2{195_JM9130013}  ikvvdleair kaeeahkade arkaeearka eeahkaeevr kaeeahkvee
   msa235427.2{195_18RS21}  ikvvdlea.. ....irkaee arkaeearka eeghktqeap iveegykvnn
     msa235427.2{195_2603}  ikvvdleair kaeearkaee arkaeearka eeghktqeap iveegykvnn
     msa235427.2{195_A909}  ikvvdleair kaeeahkade arkaeearka eearkaeear kaeeghktqe
     msa235427.2{195_COH1}  sd.ss.lrsy s.s.rst.s. rst.s.rst. s.rst.s.rs t.s.rst.sr
     msa235427.2{195_M732}  sd.ss.lrsy s.s.rst.s. rst.s.rst. s.rst.s.rs t.s.rst.sr
     msa235427.2{195_M781}  sd.ss.lrsy s.s.rst.s. rst.s.rst. s.rst.s.rs t.s.rst.sr
                 Consensus  ---------- ---------- ---------- ---------- ----------

                            1001                                              1050
     msa235427.2{195_H36B}  arkaeeghkt qeapiveegy kvnnvhqtdt tvkasdlpkt ktvsavhmar
msa235427.2{195_JM9130013}  ap.s.rgt.n prstys.rrl qg..rssn.y ys.sv.ftkd .dsfrssyg.
   msa235427.2{195_18RS21}  vhqtdttvka sdlpktktvs avhmartdnk qitshqthve ~~~~~~~~~~
     msa235427.2{195_2603}  vhqtdttvka sdlpktktvs avhmartdnk qitshqthve kqikntlpst
     msa235427.2{195_A909}  apiveegykv nnvhqtdttv kasdlpktkt vsavhmartd nkqitshqth
     msa235427.2{195_COH1}  rst.s.rgt. nprstys.rr lqs..rssn. yys.sv.ftk d.dsfrssyg
     msa235427.2{195_M732}  rst.s.rgt. nprstys.rr lqs..rssn. yys.sv.ftk d.dsfrssyg
     msa235427.2{195_M781}  rstvklkrdi kpkkhl.lkk atklitfikl ilqlkrliyq rlrqfpqfiw
                 Consensus  ---------- ---------- ---------- ---------- ----------

                            1051                          1081
     msa235427.2{195_H36B}  tdnkqitshq th~~~~~~~~ ~~~~~~~~~~ ~
msa235427.2{195_JM9130013}  nrq.tdnfts dtc~~~~~~~ ~~~~~~~~~~ ~
   msa235427.2{195_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~
     msa235427.2{195_2603}  gdskrgyyit gmaivmlsvl fslakkfksk y
     msa235427.2{195_A909}  vekqikn~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~
     msa235427.2{195_COH1}  .nrq.tdnft sdTC~~~~~~ ~~~~~~~~~~ ~
     msa235427.2{195_M732}  .nrq.tdnft sdTC.k~~~~ ~~~~~~~~~~ ~
     msa235427.2{195_M781}  leqtinr.lh irhml~~~~~ ~~~~~~~~~~ ~
                 Consensus  ---------- --******** ********** *
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Table 52: Comparative Sequences relating to SAG 1823

SEQ ID NO. 5201
STRAIN 090
AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
CAATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGA
CAACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCA
CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
CGGCGATCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCG
TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATT
CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
TATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAgAGAAAAAACCAA
ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
TATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCaGCGAA
TGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGtCTCTGCTGAAA
TGCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATT
GCTttTATTGAATCgAGTCAAGCCGAGGCTGCTAATCGtGCAaGCCACTT
ACAACAAGAAATTCTAGCATTAGATAGCCaAACGTcCGAGTATCAAATtA
AAAGTaACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAG
CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTG
GCATGTTACGTCGAAATACCATTCCAACAATGAAACTCTCAATCGCTCAG
TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
TGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAG
AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCaATTGGAATCTG
CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGAT
AAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAA
AGTTGATGAGTCT

SEQ ID NO. 5202
STRAIN A909
AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
CAATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGA
CAACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCA
CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
CGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCG
TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATT
CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
TATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAA
ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
TATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAA
TGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAA
TGCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTAwT
GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT
ACAACAAGAAATTCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA
AAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAG
CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTG
GCATGTTACGTCGAAATACCATTCCAACaATGAAACTCTCAATCGCTCAG
TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
TGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAG
AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
TATCGCTGCCATAGACAAAGGACGTAAAGAACGTGCCCAATTAGAATCTG
CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGAT
AAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAA
AGtTGATGAGTCT

SEQ ID NO. 5203
STRAIN H36B
AGCGaTACCTTTAATTTTGATATTGACCAAATTGCAGAC
AATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC
AACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTC
GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCGT
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTC
CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAAA
CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTcTCTGCTGAAAT
GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG
CTttTATTGAATCGAGTCAAGCCGAgGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTcCGAGTATCAAATTAA
AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAGC
AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG
CATGTTACGTCGAAATACCATTCCAACaATGAAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
GTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
AATCTGTCACTGCATTATCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
ATCGCTGCCATAGACAAAGGACGTAAAGAACGTGCCCAATTAGAATCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa
AAAAAATAGTTGAAGCCTTACTCAaCGAAGGTaAATCTACCCAAGAAAAA
GTTGATGAGTCT

SEQ ID NO. 5204
STRAIN 18RS21
TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAACAGATAAAA
CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
TTTTTTGAAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTCGGCGATCAAAATGCGCTCCTTGATT
TTGGACAATCCGCAGTAGAAGGCGTTAATACCACTGTTAATCATATCTTG
TCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGGCAGAATTAGAGAAAAAACCAAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATTCTAGCATTAGATA
GCCAAACGTCCGAGTATCAAATTAAAAGTAACCAATTAGCTCGAATGACT
GAAGTTATCAATACCCTCGAACAGCAACATCCTGAATATGTCAGCCGTCT
CTACGTTGCATGGGCAACAACACCACAGATGCGAAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAAACTTGGCATGTTACGTCGAAATACCATTCCA
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCaATTGGAATCTGCTGTTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTaAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5205
STRAIN M732
AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
AATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC
AACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTC
GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCGT
TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTC
CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAAA
CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAT
GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG
CTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTCCGAATATCAAATTAA
AAGTAACCAATTAGCCCGAATGACTGAAGTTATCAATACCCTCGAACAGC
AACATACGGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTGG
TATGTTACGTCGAAATACCATTCCAACAATGAAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
GTCAACGCTAATAATGCAGCATTGCAAATGCTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGC
TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA
G

SEQ ID NO. 5206
STRAIN COH1
CTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGACAACAAGCCAA
ACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCACAAAAGTCTGC
TwTCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTCGGTGACCAAA
ATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCGTTAATACTACT
GTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGA
TGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTTATTGCCAAAT
ATAAAGATGCTACTCCGGCaGAATTAGAGAAAAAACCAAACTTGATTCAA
AAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTTATTTTGACTC
ACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAATGTTGTCAAAC
AAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAATGCTCATTGAA
GATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGA
ATCGAGTCAAGCCGAgGCTGCCAATCGTGCaAGCCACTTACAACAaGAAA
TTCTAGCaTTAGATAGCCAAACGTCCGAATATCAAATTAAAAGTAACCAA
TTAGCCCGAATGACTGAaGTTATCAaTaCCCTCGAACAGCAACATACGGA
aTATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCACAGATGCGAA
ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAAACTTGGTATGTTACGT
CGAAATACCATTCCAACAATGAAACTCTCAATCGCTCAGTTAGGCATGAT
GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA
ATAATGCAGCATTGCAAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCG
ATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTAAATCTGTCAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATTATCGCTGCCA
TAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTTATTAAA
TCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATAAAAAAATAGT
TGAAGCCTTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT
CT

SEQ ID NO. 5207
STRAIN M781
TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAACAGATAAAA
CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
TTTTTTGAAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTCGGTGACCAAAATGCGCTCCTTGATT
TTGGACAATCCGCAGTAGAAGGCGTTAATACTACTGtTAATCATATCTTG
TCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGGCAGAATTAGAGAAAAAACCAAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATTCTAGCATTAGATA
GCCAAACGTCCGAATATCAAATTAAAAGTAACCAATTAGCCCGAATGACT
GAAGTTATCAATACCCTCGAACAGCAACATACGGAATATGTCAGCCGTCT
CTACGTTGCATGGGCAACAACACCACAGATGCGAAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAAACTTGGTATGTTACGTCGAAATACCATTCCA
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCAATTAGAATCTGCTGTTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208
STRAIN CJB110
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CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAATTGCC
TTTTTTGAAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTCGGCGATCAAAATGCGCTCCTTGATT
TTGGACAATCCGCAGTAGAAGGCGTTAATACCACTGTTAATCATATCTTG
TCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGGCAGAATTAGAGAAAAAACCAAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATTCTAGCATTAGATA
GCCAAACGTCCGAGTATCAAATTAAAAGTAACCAATTAGCTCGAATGACT
GAAGTTATCAATACCCTCGAACAGCAaCATACTGAATATGTCAGCCGTCT
CTACGTTGCATGGGCaACaACACCACAGATGCGAAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAAACTTGGCATGTTACGTCGAAATACCATTCCA
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTgAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAaCGTGCCCAATTGGAATCTGCTGTTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAAATTCGTGATaAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209
STRAIN 1169NT
GCAGACAATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAA
CCAGACAACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACAC
CAGCACAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACT
TTTGTCGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGA
AGGCGTTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTC
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT
GGATTTATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAA
ACCAAACTTGATCCAAAAATTATTCAAACAAAGCAAGACCTCACTACAGG
AATTTTATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCA
GCAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC
TGAAATGCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAG
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGC
CACTTACAACAAGAAATTCTAGCATTAGATAGCCAAACGTCCGAGTATCA
AATTAAAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCG
AaCAGCAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACA
aCACCACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA
ACTTGGCATGTTACGTCGAAATACCATTCCAACAATGAAACTCTCAATCG
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT
GCTATTGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT
CTATTAAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAAT
GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGA
ATCTGCTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTC
GTGATAAAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAA
GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210
STRAIN JM9130013
AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
AATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC
AACAAGCCAAACTGGGCAAATTGCCTTTTTTGAAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTC
GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAGTAGAAGGCGT
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTC
CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACCAAA
CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG
CTTTTATTGAATcGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATtAA
AAGTaACCAATTAGCTCGAATGACTGAAGTTATCAATACCCTCGAACAGC
AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG
CATGTTACGTCGAAATACCATTCCAACAATGAAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
GTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
ATCGCTGCCATAGACAAAGGaCGTAAGGAACGTGCCCAATTAGAATCTGC
TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTaAATCTACCCAAGAAAAA
GTTGATGAGTCT

SEQ ID NO. 5211
STRAIN 2603
agcgatacctttaattttgatattgaccaaattgcagacaatgctatcac
taaaacagataaaacaacagaaattatttccaaccagacaacaagccaaa
ctgggcaaattgcctttttttgaaaaactaacaccagcacaaaagtctgct
atctctgaaaaaacaccagctttggtagatacttttgtcggcgatcaaaa
tgcgctccttgattttggacaatccgcagtagaaggcgttaataccactg
ttaatcatatcttgtctgagcagaaaaaaattcaaattcctcaagttgat
gatttactaaaaaatgctaatcgcgaactaaatggatttattgccaaata
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aattattcaaacaaagcaagacctcgctacaggaattttattttgactca
caaaacatcgagcaaaaaatggatatgatggcagcgaatgttgtcaaaca
agaagatactttggcaagaaatatcgtctctgctgaaatgctcattgaag
ataatactaaatctattgaaaatttggttggagttattgcttttattgaa
tcgagtcaagccgaggctgctaatcgtgcaagccacttacaacaagaaat
tctagcattagatagccaaacgtccgagtatcaaattaaaagtaaccaat
tagctcgaatgactgaagttatcaataccctcgaacagcaacatcctgaa
tatgtcagccgtctctacgttgcatgggcaacaacaccacagatgcgaaa
cttggtcaaagtatcgtcagatatgcgtcagaaacttggcatgttacgtc
gaaataccattccaacaatgaaactctcaatcgctcagttaggcatgatg
caacaatctgtcaaatccggtgtcactgctgatgctattgtcaacgctaa
taatgcagcattgcagatgctggctgaaactagtaaagaagcgattccga
tgttagagaagaccgcacaaagccccactgtttctattaaatctgtcact
gcattagctgaaagcttagtggctcaaaataatggtattatcgctgccat
agacaaaggacgtaaggaacgtgcccaattggaatctgctgttattaaat
cggctgaaacaatcaatgattctgtcaaaattcgtgataaaaaaatagtt
gaagccttactcaacgaaggtaaatctacccaagaaaaagttgatgagtc
t

```
PRETTY of: /biotmp/msa13607.2{*}   April 22, 2002 03:55  ..

                                1                                                   50
       msa13607.2{201_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~C
       msa13607.2{201_M781}   ~~~~~~~~~~ ~~~~TTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
        msa13607.2{201_090}   AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
     msa13607.2{201_CJB110}   ~~~~~~~~~~ ~~~~TTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
     msa13607.2{201_18RS21}   ~~~~~~~~~~ ~~~~TTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
       msa13607.2{201_2603}   AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
       msa13607.2{201_A909}   AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
       msa13607.2{201_H36B}   AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
   msa13607.2{201_JM9130013}  AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
    msa13607.2{201_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~GCAGACA ATGCTATCAC
       msa13607.2{201_M732}   AGCGATACCT TTAATTTTGA TATTGACCAA ATTGCAGACA ATGCTATCAC
                  Consensus   ********** ********** ********** ********** **********
```

Table 52: Comparative Sequences relating to SAG 1823

```
                          51                                                 100
     msa13607.2{201_COH1} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
     msa13607.2{201_M781} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
      msa13607.2{201_090} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
   msa13607.2{201_CJB110} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
   msa13607.2{201_18RS21} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
     msa13607.2{201_2603} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
     msa13607.2{201_A909} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
     msa13607.2{201_H36B} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
msa13607.2{201_JM9130013} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
   msa13607.2{201_1169NT} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
     msa13607.2{201_M732} TAAAACAGAT AAAACAACAG AAATTATTTC CAACCAGACA ACAaGCCAAA
                Consensus ********** ********** ********** ********** **********

                          101                                                150
     msa13607.2{201_COH1} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
     msa13607.2{201_M781} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
      msa13607.2{201_090} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
   msa13607.2{201_CJB110} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
   msa13607.2{201_18RS21} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
     msa13607.2{201_2603} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
     msa13607.2{201_A909} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
     msa13607.2{201_H36B} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
msa13607.2{201_JM9130013} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
   msa13607.2{201_1169NT} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
     msa13607.2{201_M732} CTGGGCAAAT TGCCTTTTTT GAAAAACTAA CACCAGCACA AAAGTCTGCT
                Consensus ********** ********** ********** ********** **********

                          151                                                200
     msa13607.2{201_COH1} wTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
     msa13607.2{201_M781} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
      msa13607.2{201_090} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GcGAtCAAAA
   msa13607.2{201_CJB110} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GcGAtCAAAA
   msa13607.2{201_18RS21} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GcGAtCAAAA
     msa13607.2{201_2603} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GcGAtCAAAA
     msa13607.2{201_A909} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
     msa13607.2{201_H36B} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
msa13607.2{201_JM9130013} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
   msa13607.2{201_1169NT} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
     msa13607.2{201_M732} aTCTCTGAAA AAACACCAGC TTTGGTAGAT ACTTTTGTCG GtGAcCAAAA
                Consensus -********* ********** ********** ********** *-**-*****

                          201                                                250
     msa13607.2{201_COH1} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACtACTG
     msa13607.2{201_M781} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACtACTG
      msa13607.2{201_090} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
   msa13607.2{201_CJB110} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
   msa13607.2{201_18RS21} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
     msa13607.2{201_2603} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
     msa13607.2{201_A909} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
     msa13607.2{201_H36B} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
msa13607.2{201_JM9130013} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
   msa13607.2{201_1169NT} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACcACTG
     msa13607.2{201_M732} TGCGCTCCTT GATTTTGGAC AATCCGCAGT AGAAGGCGTT AATACtACTG
                Consensus ********** ********** ********** ********** *****-****

                          251                                                300
     msa13607.2{201_COH1} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
     msa13607.2{201_M781} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
      msa13607.2{201_090} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
   msa13607.2{201_CJB110} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
   msa13607.2{201_18RS21} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
     msa13607.2{201_2603} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
     msa13607.2{201_A909} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
     msa13607.2{201_H36B} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
msa13607.2{201_JM9130013} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
   msa13607.2{201_1169NT} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
     msa13607.2{201_M732} TTAATCATAT CTTGTCTGAG CAGAAAAAAA TTCAAATTCC TCAAGTTGAT
                Consensus ********** ********** ********** ********** **********

                          301                                                350
     msa13607.2{201_COH1} GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
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Table 52: Comparative Sequences relating to SAG 1823

```
     msa13607.2{201_M781}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
      msa13607.2{201_090}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
   msa13607.2{201_CJB110}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
   msa13607.2{201_18RS21}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
     msa13607.2{201_2603}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
     msa13607.2{201_A909}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
     msa13607.2{201_H36B}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
msa13607.2{201_JM9130013}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
   msa13607.2{201_1169NT}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
     msa13607.2{201_M732}  GATTTACTAA AAAATGCTAA TCGCGAACTA AATGGATTTA TTGCCAAATA
                Consensus  ********** ********** ********** ********** **********

                           351                                              400
     msa13607.2{201_COH1}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
     msa13607.2{201_M781}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
      msa13607.2{201_090}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
   msa13607.2{201_CJB110}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
   msa13607.2{201_18RS21}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
     msa13607.2{201_2603}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
     msa13607.2{201_A909}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
     msa13607.2{201_H36B}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
msa13607.2{201_JM9130013}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
   msa13607.2{201_1169NT}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATcCAAA
     msa13607.2{201_M732}  TAAAGATGCT ACTCCGGCAG AATTAGAGAA AAAACCAAAC TTGATtCAAA
                Consensus  ********** ********** ********** ********** *****-****

                           401                                              450
     msa13607.2{201_COH1}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
     msa13607.2{201_M781}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
      msa13607.2{201_090}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
   msa13607.2{201_CJB110}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
   msa13607.2{201_18RS21}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
     msa13607.2{201_2603}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
     msa13607.2{201_A909}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
     msa13607.2{201_H36B}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
msa13607.2{201_JM9130013}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
   msa13607.2{201_1169NT}  AATTATTCAA ACAAAGCAAG ACCTCaCTAC AGGAATTTTA TTTTGACTCA
     msa13607.2{201_M732}  AATTATTCAA ACAAAGCAAG ACCTCgCTAC AGGAATTTTA TTTTGACTCA
                Consensus  ********** ********** *****-**** ********** **********

                           451                                              500
     msa13607.2{201_COH1}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCaAATG TTGTCAAACA
     msa13607.2{201_M781}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCaAATG TTGTCAAACA
      msa13607.2{201_090}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
   msa13607.2{201_CJB110}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
   msa13607.2{201_18RS21}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
     msa13607.2{201_2603}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
     msa13607.2{201_A909}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
     msa13607.2{201_H36B}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
msa13607.2{201_JM9130013}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCgAATG TTGTCAAACA
   msa13607.2{201_1169NT}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCaAATG TTGTCAAACA
     msa13607.2{201_M732}  CAAAACATCG AGCAAAAAAT GGATATGATG GCAGCaAATG TTGTCAAACA
                Consensus  ********** ********** ********** *****-**** **********

                           501                                              550
     msa13607.2{201_COH1}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
     msa13607.2{201_M781}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
      msa13607.2{201_090}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
   msa13607.2{201_CJB110}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
   msa13607.2{201_18RS21}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
     msa13607.2{201_2603}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
     msa13607.2{201_A909}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
     msa13607.2{201_H36B}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
msa13607.2{201_JM9130013}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
   msa13607.2{201_1169NT}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
     msa13607.2{201_M732}  AGAAGATACT TTGGCAAGAA ATATCGTCTC TGCTGAAATG CTCATTGAAG
                Consensus  ********** ********** ********** ********** **********

                           551                                              600
     msa13607.2{201_COH1}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
     msa13607.2{201_M781}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
      msa13607.2{201_090}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
   msa13607.2{201_CJB110}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
   msa13607.2{201_18RS21}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
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Table 52: Comparative Sequences relating to SAG 1823

```
      msa13607.2{201_2603}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
      msa13607.2{201_A909}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAwTGC TTTTATTGAA
      msa13607.2{201_H36B}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
 msa13607.2{201_JM9130013}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
    msa13607.2{201_1169NT}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
      msa13607.2{201_M732}  ATAATACTAA ATCTATTGAA AATTTGGTTG GAGTTAtTGC TTTTATTGAA
                 Consensus  ********** ********** ********** ******-*** **********

                            601                                                650
      msa13607.2{201_COH1}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
      msa13607.2{201_M781}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
       msa13607.2{201_090}  TCGAGTCAAG CCGAGGCTGC tAATCGTGCA AGCCACTTAC AACAAGAAAT
    msa13607.2{201_CJB110}  TCGAGTCAAG CCGAGGCTGC tAATCGTGCA AGCCACTTAC AACAAGAAAT
    msa13607.2{201_18RS21}  TCGAGTCAAG CCGAGGCTGC tAATCGTGCA AGCCACTTAC AACAAGAAAT
      msa13607.2{201_2603}  TCGAGTCAAG CCGAGGCTGC tAATCGTGCA AGCCACTTAC AACAAGAAAT
      msa13607.2{201_A909}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
      msa13607.2{201_H36B}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
 msa13607.2{201_JM9130013}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
    msa13607.2{201_1169NT}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
      msa13607.2{201_M732}  TCGAGTCAAG CCGAGGCTGC cAATCGTGCA AGCCACTTAC AACAAGAAAT
                 Consensus  ********** ********** -********* ********** **********

                            651                                                700
      msa13607.2{201_COH1}  TCTAGCATTA GATAGCCAAA CGTCCGAaTA TCAAATTAAA AGTAACCAAT
      msa13607.2{201_M781}  TCTAGCATTA GATAGCCAAA CGTCCGAaTA TCAAATTAAA AGTAACCAAT
       msa13607.2{201_090}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
    msa13607.2{201_CJB110}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
    msa13607.2{201_18RS21}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
      msa13607.2{201_2603}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
      msa13607.2{201_A909}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
      msa13607.2{201_H36B}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
 msa13607.2{201_JM9130013}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
    msa13607.2{201_1169NT}  TCTAGCATTA GATAGCCAAA CGTCCGAgTA TCAAATTAAA AGTAACCAAT
      msa13607.2{201_M732}  TCTAGCATTA GATAGCCAAA CGTCCGAaTA TCAAATTAAA AGTAACCAAT
                 Consensus  ********** ********** *******-** ********** **********

                            701                                                750
      msa13607.2{201_COH1}  TAGCcCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCgGAA
      msa13607.2{201_M781}  TAGCcCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCgGAA
       msa13607.2{201_090}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
    msa13607.2{201_CJB110}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
    msa13607.2{201_18RS21}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATcCtGAA
      msa13607.2{201_2603}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATcCtGAA
      msa13607.2{201_A909}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
      msa13607.2{201_H36B}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
 msa13607.2{201_JM9130013}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
    msa13607.2{201_1169NT}  TAGCtCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCtGAA
      msa13607.2{201_M732}  TAGCcCGAAT GACTGAAGTT ATCAATACCC TCGAACAGCA ACATaCgGAA
                 Consensus  ****-***** ********** ********** ********** ****-*-***

                            751                                                800
      msa13607.2{201_COH1}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
      msa13607.2{201_M781}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
       msa13607.2{201_090}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
    msa13607.2{201_CJB110}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
    msa13607.2{201_18RS21}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
      msa13607.2{201_2603}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
      msa13607.2{201_A909}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
      msa13607.2{201_H36B}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
 msa13607.2{201_JM9130013}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
    msa13607.2{201_1169NT}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
      msa13607.2{201_M732}  TATGTCAGCC GTCTCTACGT TGCATGGGCA ACAACACCAC AGATGCGAAA
                 Consensus  ********** ********** ********** ********** **********

                            801                                                850
      msa13607.2{201_COH1}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGt ATGTTACGTC
      msa13607.2{201_M781}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGt ATGTTACGTC
       msa13607.2{201_090}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGc ATGTTACGTC
    msa13607.2{201_CJB110}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGc ATGTTACGTC
    msa13607.2{201_18RS21}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGc ATGTTACGTC
      msa13607.2{201_2603}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGc ATGTTACGTC
      msa13607.2{201_A909}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA aAAACTTGGc ATGTTACGTC
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Table 52: Comparative Sequences relating to SAG 1823

```
      msa13607.2{201_H36B}   CTTGGTCAAA GTATCGTCAG ATATGCGTCA aAAACTTGGc ATGTTACGTC
  msa13607.2{201_JM9130013}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA aAAACTTGGc ATGTTACGTC
     msa13607.2{201_1169NT}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA aAAACTTGGc ATGTTACGTC
       msa13607.2{201_M732}  CTTGGTCAAA GTATCGTCAG ATATGCGTCA gAAACTTGGt ATGTTACGTC
                  Consensus  ********** ********** ********** -********- **********

                             851                                                900
       msa13607.2{201_COH1}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
       msa13607.2{201_M781}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
        msa13607.2{201_090}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
     msa13607.2{201_CJB110}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
     msa13607.2{201_18RS21}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
       msa13607.2{201_2603}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
       msa13607.2{201_A909}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
       msa13607.2{201_H36B}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
  msa13607.2{201_JM9130013}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
     msa13607.2{201_1169NT}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
       msa13607.2{201_M732}  GAAATACCAT TCCAACAATG AAACTCTCAA TCGCTCAGTT AGGCATGATG
                  Consensus  ********** ********** ********** ********** **********

                             901                                                950
       msa13607.2{201_COH1}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
       msa13607.2{201_M781}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
        msa13607.2{201_090}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
     msa13607.2{201_CJB110}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
     msa13607.2{201_18RS21}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
       msa13607.2{201_2603}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
       msa13607.2{201_A909}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
       msa13607.2{201_H36B}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
  msa13607.2{201_JM9130013}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
     msa13607.2{201_1169NT}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
       msa13607.2{201_M732}  CAACAATCTG TCAAATCCGG TGTCACTGCT GATGCTATTG TCAACGCTAA
                  Consensus  ********** ********** ********** ********** **********

                             951                                               1000
       msa13607.2{201_COH1}  TAATGCAGCA TTGCAaATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
       msa13607.2{201_M781}  TAATGCAGCA TTGCAaATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
        msa13607.2{201_090}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
     msa13607.2{201_CJB110}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
     msa13607.2{201_18RS21}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
       msa13607.2{201_2603}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
       msa13607.2{201_A909}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
       msa13607.2{201_H36B}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
  msa13607.2{201_JM9130013}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
     msa13607.2{201_1169NT}  TAATGCAGCA TTGCAgATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
       msa13607.2{201_M732}  TAATGCAGCA TTGCAaATGC TGGCTGAAAC TAGTAAAGAA GCGATTCCGA
                  Consensus  ********** *****-**** ********** ********** **********

                             1001                                              1050
       msa13607.2{201_COH1}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
       msa13607.2{201_M781}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
        msa13607.2{201_090}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
     msa13607.2{201_CJB110}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
     msa13607.2{201_18RS21}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
       msa13607.2{201_2603}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
       msa13607.2{201_A909}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
       msa13607.2{201_H36B}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
  msa13607.2{201_JM9130013}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
     msa13607.2{201_1169NT}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
       msa13607.2{201_M732}  TGTTAGAGAA GACCGCACAA AGCCCCACTG TTTCTATTAA ATCTGTCACT
                  Consensus  ********** ********** ********** ********** **********

                             1051                                              1100
       msa13607.2{201_COH1}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
       msa13607.2{201_M781}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
        msa13607.2{201_090}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
     msa13607.2{201_CJB110}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
     msa13607.2{201_18RS21}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
       msa13607.2{201_2603}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
       msa13607.2{201_A909}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
       msa13607.2{201_H36B}  GCATTAtCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
  msa13607.2{201_JM9130013}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
     msa13607.2{201_1169NT}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
```

Table 52: Comparative Sequences relating to SAG 1823

```
    msa13607.2{201_M732}  GCATTAgCTG AAAGCTTAGT GGCTCAAAAT AATGGTATTA TCGCTGCCAT
               Consensus  ******-*** ********** ********** ********** **********

                          1101                                              1150
    msa13607.2{201_COH1}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
    msa13607.2{201_M781}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
     msa13607.2{201_090}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT gGAATCTGCT GTTATTAAAT
  msa13607.2{201_CJB110}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT gGAATCTGCT GTTATTAAAT
  msa13607.2{201_18RS21}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT gGAATCTGCT GTTATTAAAT
    msa13607.2{201_2603}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT gGAATCTGCT GTTATTAAAT
    msa13607.2{201_A909}  AGACAAAGGA CGTAAaGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
    msa13607.2{201_H36B}  AGACAAAGGA CGTAAaGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
msa13607.2{201_JM9130013}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
  msa13607.2{201_1169NT}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
    msa13607.2{201_M732}  AGACAAAGGA CGTAAgGAAC GTGCCCAATT aGAATCTGCT GTTATTAAAT
               Consensus  ********** *****-**** ********** -********* **********

                          1151                                              1200
    msa13607.2{201_COH1}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
    msa13607.2{201_M781}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
     msa13607.2{201_090}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
  msa13607.2{201_CJB110}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
  msa13607.2{201_18RS21}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
    msa13607.2{201_2603}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
    msa13607.2{201_A909}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
    msa13607.2{201_H36B}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
msa13607.2{201_JM9130013}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
  msa13607.2{201_1169NT}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
    msa13607.2{201_M732}  CGGCTGAAAC AATCAATGAT TCTGTCAAAA TTCGTGATAA AAAAATAGTT
               Consensus  ********** ********** ********** ********** **********

                          1201                                              1250
    msa13607.2{201_COH1}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
    msa13607.2{201_M781}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
     msa13607.2{201_090}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
  msa13607.2{201_CJB110}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
  msa13607.2{201_18RS21}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
    msa13607.2{201_2603}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
    msa13607.2{201_A909}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
    msa13607.2{201_H36B}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
msa13607.2{201_JM9130013}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
  msa13607.2{201_1169NT}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ttgatgagtc
    msa13607.2{201_M732}  GAAGCCTTAC TCAACGAAGG TAAATCTACC CAAGAAAAAG ~~~~~~~~~~
               Consensus  ********** ********** ********** ********** ----------

                          1251
    msa13607.2{201_COH1}  t
    msa13607.2{201_M781}  t
     msa13607.2{201_090}  t
  msa13607.2{201_CJB110}  t
  msa13607.2{201_18RS21}  t
    msa13607.2{201_2603}  t
    msa13607.2{201_A909}  t
    msa13607.2{201_H36B}  t
msa13607.2{201_JM9130013}  t
  msa13607.2{201_1169NT}  t
    msa13607.2{201_M732}  ~
               Consensus  -
```

SEQ ID NO. 5212
STRAIN _090 frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 52013
STRAIN A909 frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LIEDNTKSIENLVGVXAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5214
STRAIN H36B frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALSESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5215
STRAIN 18RS21 frame: 2
FDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5216
STRAIN M732 frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEK

SEQ ID NO. 5217
STRAIN COH1 frame: 3
KTDKTTEIISNQTTCQTGQIAFFEKLTPAQKSAXSEKTPALVDTFVGDQNALLDFGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA
FIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN
NAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQL
ESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5218
STRAIN COH1 frame: 3
KTDKTTEIISNQTTCQTGQIAFFEKLTPAQKSAXSEKTPALVDTFVGDQNALLDFGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA
FIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN
NAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQL
ESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5219
STRAIN M781 frame: 2
FDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5220
STRAIN CJB110 frame: 2
FDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDN
TKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5221
STRAIN 1169NT frame: 1
ADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVDTFVGDQNALLD
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNL
IQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIEN
LVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY
VSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD
AIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

```
KERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222
STRAIN JM9130013 frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223
STRAIN 2603 frame: 1
SDTFNFDIDQIADNAITKTDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEAANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{*}   April 22, 2002 04:27  ..

                           1                                                   50
      msa28369.2{201_090}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
   msa28369.2{201_1169NT}  ~~~~~~~~~~ ~adnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_A909}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
msa28369.2{201_JM9130013}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_COH1}  ~~~~~~~~~~ ~~~~~~~KTD KTTEIISNQT TcQTGQIAFF EKLTPAQKSA
   msa28369.2{201_CJB110}  ~~~~~fdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_M781}  ~~~~~fdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_2603}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_H36B}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
   msa28369.2{201_18RS21}  ~~~~~fdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
     msa28369.2{201_M732}  sdtfnfdidq iadnaitKTD KTTEIISNQT TsQTGQIAFF EKLTPAQKSA
                Consensus  ---------- -------*** ********** *-******** **********

                           51                                                 100
      msa28369.2{201_090}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
   msa28369.2{201_1169NT}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_A909}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
msa28369.2{201_JM9130013}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_COH1}  xSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
   msa28369.2{201_CJB110}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_M781}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_2603}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_H36B}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
   msa28369.2{201_18RS21}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
     msa28369.2{201_M732}  iSEKTPALVD TFVGDQNALL DFGQSAVEGV NTTVNHILSE QKKIQIPQVD
                Consensus  -********* ********** ********** ********** **********

                           101                                                150
      msa28369.2{201_090}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
   msa28369.2{201_1169NT}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_A909}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
msa28369.2{201_JM9130013}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_COH1}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
   msa28369.2{201_CJB110}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_M781}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_2603}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_H36B}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
   msa28369.2{201_18RS21}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
     msa28369.2{201_M732}  DLLKNANREL NGFIAKYKDA TPAELEKKPN LIQKLFKQSK TSLQEFYFDS
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
      msa28369.2{201_090}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
   msa28369.2{201_1169NT}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
     msa28369.2{201_A909}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGVxAFIE
msa28369.2{201_JM9130013}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
     msa28369.2{201_COH1}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
   msa28369.2{201_CJB110}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
     msa28369.2{201_M781}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
     msa28369.2{201_2603}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
     msa28369.2{201_H36B}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
```

Table 52: Comparative Sequences relating to SAG 1823

```
    msa28369.2{201_18RS21}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
      msa28369.2{201_M732}  QNIEQKMDMM AANVVKQEDT LARNIVSAEM LIEDNTKSIE NLVGViAFIE
                 Consensus  ********** ********** ********** ********** *****-****

                            201                                                250
       msa28369.2{201_090}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
    msa28369.2{201_1169NT}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
      msa28369.2{201_A909}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
  msa28369.2{201_JM9130013}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
      msa28369.2{201_COH1}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
    msa28369.2{201_CJB110}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
      msa28369.2{201_M781}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
      msa28369.2{201_2603}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHpE
      msa28369.2{201_H36B}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
    msa28369.2{201_18RS21}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHpE
      msa28369.2{201_M732}  SSQAEAANRA SHLQQEILAL DSQTSEYQIK SNQLARMTEV INTLEQQHtE
                 Consensus  ********** ********** ********** ********** ********-*

                            251                                                300
       msa28369.2{201_090}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
    msa28369.2{201_1169NT}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_A909}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
  msa28369.2{201_JM9130013}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_COH1}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
    msa28369.2{201_CJB110}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_M781}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_2603}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_H36B}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
    msa28369.2{201_18RS21}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
      msa28369.2{201_M732}  YVSRLYVAWA TTPQMRNLVK VSSDMRQKLG MLRRNTIPTM KLSIAQLGMM
                 Consensus  ********** ********** ********** ********** **********

                            301                                                350
       msa28369.2{201_090}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
    msa28369.2{201_1169NT}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_A909}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
  msa28369.2{201_JM9130013}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_COH1}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
    msa28369.2{201_CJB110}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_M781}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_2603}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_H36B}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
    msa28369.2{201_18RS21}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
      msa28369.2{201_M732}  QQSVKSGVTA DAIVNANNAA LQMLAETSKE AIPMLEKTAQ SPTVSIKSVT
                 Consensus  ********** ********** ********** ********** **********

                            351                                                400
       msa28369.2{201_090}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
    msa28369.2{201_1169NT}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_A909}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
  msa28369.2{201_JM9130013}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_COH1}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
    msa28369.2{201_CJB110}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_M781}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_2603}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_H36B}  ALsESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
    msa28369.2{201_18RS21}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
      msa28369.2{201_M732}  ALaESLVAQN NGIIAAIDKG RKERAQLESA VIKSAETIND SVKIRDKKIV
                 Consensus  **-******* ********** ********** ********** **********

                            401        417
       msa28369.2{201_090}  EALLNEGKST QEKvdes
    msa28369.2{201_1169NT}  EALLNEGKST QEKvdes
      msa28369.2{201_A909}  EALLNEGKST QEKvdes
  msa28369.2{201_JM9130013}  EALLNEGKST QEKvdes
      msa28369.2{201_COH1}  EALLNEGKST QEKvdes
    msa28369.2{201_CJB110}  EALLNEGKST QEKvdes
      msa28369.2{201_M781}  EALLNEGKST QEKvdes
      msa28369.2{201_2603}  EALLNEGKST QEKvdes
      msa28369.2{201_H36B}  EALLNEGKST QEKvdes
    msa28369.2{201_18RS21}  EALLNEGKST QEKvdes
      msa28369.2{201_M732}  EALLNEGKST QEK~~~~
                 Consensus  ********** ***----
```

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5301
STRAIN 2603
acaaatactttgaaaaaagaattagttgaagctaaaaagacaattccatc
cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag
agtttgttcttaaaccgattatcgatgtctctggttggcaacttcctaag
gagattgattacgatacgctttcaaaaaatatttcaggtgttgttattcg
tgtctttggtggatcaaagatatctaagactaataacgctgcttatacaa
ctggaatcgataaatcgtttaagacccatatcaaagaatttcaaaagcga
aatatcccagtagctgtctacagttatgcacttggttcaagtgttaaaga
aatgaaagaagaggctcagatattttataagaatgcagctccttacaaac
caactttttattggattgacgtagaagaggagacaatgtctaacatgaat
aaaggtgtccaagcattccgaaaagaattaaaaagacttggtgctaaaaa
tgttggtatctacattggtacttactttatgactgagcaaggcatctctg
taaaaggatttgacgctgtttggattccaacttatggtagcgattctgga
tactatgaagcggctccgcaaactgaacttaaatacgatttacaccaata
cacctctcaaggttatctaccaggawtcaatcaaccgcttgatttaaatc
aaattgcagttaataaagacaagaagaaaacttatgagaaactttttgga
aaagtaaaagag

SEQ ID NO. 5302
STRAIN 090
ACAAATACTTTGAAAAAAGAATTAG
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAGGTGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC
CCATATCAAAGAATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTT
ATGCACTTGGTTCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
TCCAACTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAAACTTATGAGAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5303
STRAIN A909
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA
AGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCA
TCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTTG
GCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAG
GTGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
GCTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGA
ATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGTT
CAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCA
GCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAAT
GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGAC
TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG
CAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATGG
TAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACG
ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
CTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATGA
GAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5304
STRAIN H36B
ACAAATACTTTGAAAAAAGAATTAG
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAGGTGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC
CCATATCAAAGAATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTT
ATGCACTTGGTTCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
TCCAACTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAAACTTATGAGAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5305
STRAIN 18RS21
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAAA
GACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCAT
CGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGG
CAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAGG
TGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGAA
TTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGTTC
AAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAG
CTCCTTACAAACCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAATG
TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACT
TGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC
AAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATGGT
AGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACGA
TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC
TTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATGAG
AAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5306
STRAIN M732
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAA
AAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATC
ATCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTT
GGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA
GGTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAG
AATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGT
TCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGC
AGCTCCTTACAAaCCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAA
TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA
CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATG
GTAGCGATTCTGGATACTATGAAGCAGCTCCACAAACTGAACTTAAATAC
GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATG
AGAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5307
STRAIN COH1
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA
AGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCA
TCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTTG
GCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAG
GTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
GCTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGA
ATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGTT
CAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCA
GCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAAT
GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGAC
TTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG
CAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATGG
TAGCGATTCTGGATACTATGAAGCAGCTCCACAAACTGAACTTAAATACG
ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
CTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATGA
GAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5308
STRAIN M781
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAA
AAGACAATTCCATCcGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATC
ATCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTT
GGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA
GGTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
CGCTGCTTATACAACTGGAATCGATAAATcGTTTAAGACCCATATCAAAG
AATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGT
TCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGC
AGCTCCTTACAAACCAACTTTTTatTGGATTGACGTAGAAGAGGAGaCAA
TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA
CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATG
GTAGCGATTCTGGATACTATGAAGCAGCTCCACAAACTGAACTTAAATAC
GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATG
AGAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5309
STRAIN CJB110
AAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCCATCCG
TAAAAGCTTCAAAAGTACCGCAAAAATCAACATCATCGAAAGATAAAGAG
TTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCTAAGGA
GATTGATTACGATACGCTTTCAAAAAATATTTCAGGTGTTGTTATTCGTG
TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATACAACT
GGAATCGATAAATCGTTTAAGACCCATATCAAAGAATTTCAAAAGCGAAA
TATCCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTTAAAGAAA
TGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAGCTCCTTACAAACCA
ACTTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA
AGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACTTGGTGCTAAAAATG
TTGGTATCTACATTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA
AAAGGATTTGACGCTGTTTGGATTCCAACTTATGGTAGCGATTCTGGATA

Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACTTAAATACGATTTACACCAATACA
CCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAAATCAA
ATTACAGTTAATAAAGACAAGAAGAAAACTTATGAGAAACTTTTTGGAAA
AGTAAAAGAG

SEQ ID NO. 5310
STRAIN 1169NT
ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCC
ATCCGTAAAAGCTTCAAAAGTACCGCAAAAATCAACATCATCGAAAGATA
AAGAGTTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCT
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAGGTGTTGTTAT
TCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATA
CAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGAATTTCAAAAG
CGAAATATCCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTTAA
AGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCAGCTCCTTACA
AACCAACTTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATG
AATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACTTGGCGCTAA
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT
CTGTAAAAGGATTTGACGCTGTTTGGATTCCAACTTATGGTAGCGATTCT
GGATACTATGAAGCAGCTCCGCAAACTGAACTTAAATACGATTTACACCA
ATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAA
ATCAAATTGCAGTTAATAAAGACAAGAAGAAAACTTATGAGAAACTTTTT
GGAAAAGTAAAAGAG

SEQ ID NO. 5311
STRAIN JM9130013
ACAAATACTTTGAAAAAAGAATTAG
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAGGTGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC
CCATATCAAAGAATTTCAAAAGCGAAATATCCCAGTAGCTGTCTACAGTT
ATGCACTTGGTTCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTTGACGCTGTTTGGAT
TCCAACTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAAACTTATGAGAAACTTTTTGGAAAAGTAAAAGAG

```
PRETTY of: /biotmp/msa21441.2{*}   January 20, 2003 03:46 ..

                         1                                                50
       msa21441.2{206_090}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
     msa21441.2{206_18RS21}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_2603}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_A909}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_H36B}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
 msa21441.2{206_JM9130013}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
    msa21441.2{206_CJB110}  --AAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_COH1}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_M732}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
      msa21441.2{206_M781}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
    msa21441.2{206_1169NT}  acAAATACTT TGAAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATTCCATC
                 Consensus  --******** ********** ********** ********** **********

                         51                                              100
       msa21441.2{206_090}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
     msa21441.2{206_18RS21}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_2603}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_A909}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_H36B}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
 msa21441.2{206_JM9130013}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
    msa21441.2{206_CJB110}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_COH1}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_M732}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
      msa21441.2{206_M781}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
    msa21441.2{206_1169NT}  CGTAAAAGCT TCAAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
                 Consensus  ********** ********** ********** ********** **********

                         101                                             150
       msa21441.2{206_090}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
     msa21441.2{206_18RS21}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
      msa21441.2{206_2603}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
      msa21441.2{206_A909}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
      msa21441.2{206_H36B}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
 msa21441.2{206_JM9130013}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
    msa21441.2{206_CJB110}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
      msa21441.2{206_COH1}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
      msa21441.2{206_M732}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
```

Table 53: Comparative Sequences relating to SAG 0755

```
     msa21441.2{206_M781}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
   msa21441.2{206_1169NT}  AGTTTGTTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
      msa21441.2{206_090}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
   msa21441.2{206_18RS21}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_2603}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_A909}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_H36B}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
msa21441.2{206_JM9130013}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
   msa21441.2{206_CJB110}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_COH1}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_M732}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
     msa21441.2{206_M781}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
   msa21441.2{206_1169NT}  GAGATTGATT ACGATACGCT TTCAAAAAAT ATTTCAGGTG TTGTTATTCG
                Consensus  ********** ********** ********** ********** **********

                           201                                                250
      msa21441.2{206_090}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
   msa21441.2{206_18RS21}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_2603}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_A909}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_H36B}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
msa21441.2{206_JM9130013}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
   msa21441.2{206_CJB110}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_COH1}  TaTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_M732}  TaTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
     msa21441.2{206_M781}  TaTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
   msa21441.2{206_1169NT}  TgTCTTTGGT GGATCAAAGA TATCTAAGAC TAATAACGCT GCTTATACAA
                Consensus  *-******** ********** ********** ********** **********

                           251                                                300
      msa21441.2{206_090}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
   msa21441.2{206_18RS21}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_2603}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_A909}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_H36B}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
msa21441.2{206_JM9130013}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
   msa21441.2{206_CJB110}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_COH1}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_M732}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
     msa21441.2{206_M781}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
   msa21441.2{206_1169NT}  CTGGAATCGA TAAATCGTTT AAGACCCATA TCAAAGAATT TCAAAAGCGA
                Consensus  ********** ********** ********** ********** **********

                           301                                                350
      msa21441.2{206_090}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
   msa21441.2{206_18RS21}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_2603}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_A909}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_H36B}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
msa21441.2{206_JM9130013}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
   msa21441.2{206_CJB110}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_COH1}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_M732}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
     msa21441.2{206_M781}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
   msa21441.2{206_1169NT}  AATATCCCAG TAGCTGTCTA CAGTTATGCA CTTGGTTCAA GTGTTAAAGA
                Consensus  ********** ********** ********** ********** **********

                           351                                                400
      msa21441.2{206_090}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
   msa21441.2{206_18RS21}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_2603}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_A909}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_H36B}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
msa21441.2{206_JM9130013}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
   msa21441.2{206_CJB110}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_COH1}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_M732}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
     msa21441.2{206_M781}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
   msa21441.2{206_1169NT}  AATGAAAGAA GAGGCTCAGA TATTTTATAA GAATGCAGCT CCTTACAAAC
                Consensus  ********** ********** ********** ********** **********

                           401                                                450
      msa21441.2{206_090}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
   msa21441.2{206_18RS21}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
     msa21441.2{206_2603}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
     msa21441.2{206_A909}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
     msa21441.2{206_H36B}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
msa21441.2{206_JM9130013}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
   msa21441.2{206_CJB110}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
     msa21441.2{206_COH1}  CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
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Table 53: Comparative Sequences relating to SAG 0755

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       msa21441.2{206_M732}   CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
       msa21441.2{206_M781}   CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
     msa21441.2{206_1169NT}   CAACTTTTTA TTGGATTGAC GTAGAAGAGG AGACAATGTC TAACATGAAT
                  Consensus   ********** ********** ********** ********** **********

                              451                                                500
        msa21441.2{206_090}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
     msa21441.2{206_18RS21}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_2603}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_A909}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_H36B}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
   msa21441.2{206_JM9130013}  AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
     msa21441.2{206_CJB110}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_COH1}   AAAGGTGTCC AAGCATTCCG AAAAGAgTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_M732}   AAAGGTGTCC AAGCATTCCG AAAAGAgTTA AAAAGACTTG GtGCTAAAAA
       msa21441.2{206_M781}   AAAGGTGTCC AAGCATTCCG AAAAGAgTTA AAAAGACTTG GtGCTAAAAA
     msa21441.2{206_1169NT}   AAAGGTGTCC AAGCATTCCG AAAAGAaTTA AAAAGACTTG GcGCTAAAAA
                  Consensus   ********** ********** ******_*** ********** *_********

                              501                                                550
        msa21441.2{206_090}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
     msa21441.2{206_18RS21}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
       msa21441.2{206_2603}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
       msa21441.2{206_A909}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
       msa21441.2{206_H36B}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
   msa21441.2{206_JM9130013}  TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
     msa21441.2{206_CJB110}   TGTTGGTATC TACATtGGTA CTTACTTTAT GACTGAGCAA GGcATCTCTG
       msa21441.2{206_COH1}   TGTTGGTATC TACATcGGTA CTTACTTTAT GACTGAGCAA GGtATCTCTG
       msa21441.2{206_M732}   TGTTGGTATC TACATcGGTA CTTACTTTAT GACTGAGCAA GGtATCTCTG
       msa21441.2{206_M781}   TGTTGGTATC TACATcGGTA CTTACTTTAT GACTGAGCAA GGtATCTCTG
     msa21441.2{206_1169NT}   TGTTGGTATC TACATcGGTA CTTACTTTAT GACTGAGCAA GGtATCTCTG
                  Consensus   ********** *****_**** ********** ********** **_*******

                              551                                                600
        msa21441.2{206_090}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
     msa21441.2{206_18RS21}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_2603}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_A909}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_H36B}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
   msa21441.2{206_JM9130013}  TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
     msa21441.2{206_CJB110}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_COH1}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_M732}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
       msa21441.2{206_M781}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
     msa21441.2{206_1169NT}   TAAAAGGATT TGACGCTGTT TGGATTCCAA CTTATGGTAG CGATTCTGGA
                  Consensus   ********** ********** ********** ********** **********

                              601                                                650
        msa21441.2{206_090}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
     msa21441.2{206_18RS21}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_2603}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_A909}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_H36B}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
   msa21441.2{206_JM9130013}  TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
     msa21441.2{206_CJB110}   TACTATGAAG CgGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_COH1}   TACTATGAAG CaGCTCCaCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_M732}   TACTATGAAG CaGCTCCaCA AACTGAACTT AAATACGATT TACACCAATA
       msa21441.2{206_M781}   TACTATGAAG CaGCTCCaCA AACTGAACTT AAATACGATT TACACCAATA
     msa21441.2{206_1169NT}   TACTATGAAG CaGCTCCgCA AACTGAACTT AAATACGATT TACACCAATA
                  Consensus   ********** *_*****_** ********** ********** **********

                              651                                                700
        msa21441.2{206_090}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
     msa21441.2{206_18RS21}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_2603}   CACCTCTCAA GGTTATCTAC CAGGAwTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_A909}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_H36B}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
   msa21441.2{206_JM9130013}  CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
     msa21441.2{206_CJB110}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_COH1}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_M732}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
       msa21441.2{206_M781}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
     msa21441.2{206_1169NT}   CACCTCTCAA GGTTATCTAC CAGGAtTCAA TCAACCGCTT GATTTAAATC
                  Consensus   ********** ********** *****_**** ********** **********

                              701                                                750
        msa21441.2{206_090}   AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
     msa21441.2{206_18RS21}   AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
       msa21441.2{206_2603}   AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
       msa21441.2{206_A909}   AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
       msa21441.2{206_H36B}   AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
   msa21441.2{206_JM9130013}  AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
     msa21441.2{206_CJB110}   AAATTaCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
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Table 53: Comparative Sequences relating to SAG 0755

```
     msa21441.2{206_COH1}  AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
     msa21441.2{206_M732}  AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
     msa21441.2{206_M781}  AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
   msa21441.2{206_1169NT}  AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTTGGA
                Consensus  *****-**** ********** ********** ********** **********

                           751        762
      msa21441.2{206_090}  AAAGTAAAAG AG
    msa21441.2{206_18RS21}  AAAGTAAAAG AG
     msa21441.2{206_2603}  AAAGTAAAAG AG
     msa21441.2{206_A909}  AAAGTAAAAG AG
     msa21441.2{206_H36B}  AAAGTAAAAG AG
msa21441.2{206_JM9130013}  AAAGTAAAAG AG
   msa21441.2{206_CJB110}  AAAGTAAAAG AG
     msa21441.2{206_COH1}  AAAGTAAAAG AG
     msa21441.2{206_M732}  AAAGTAAAAG AG
     msa21441.2{206_M781}  AAAGTAAAAG AG
   msa21441.2{206_1169NT}  AAAGTAAAAG AG
                Consensus  ********** **
```

SEQ ID NO. 5312
STRAIN 2603 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGXNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5313
STRAIN 090 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5314
STRAIN A909 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5315
STRAIN H36B frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5316
STRAIN 18RS21 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5317
STRAIN M732 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5318
STRAIN COH1 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5319
STRAIN M781 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5320
STRAIN CJB110 frame: 2
NTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKNI
SGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKEE
AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQG
ISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQITVNKDK
KKTYEKLFGKVKE

SEQ ID NO. 5321
STRAIN 1169NT frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

SEQ ID NO. 5322
STRAIN JM9130013 frame: 1
TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIPVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVQAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDAVWIPTYGSDSGYYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
KKKTYEKLFGKVKE

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 PRETTY of: /biotmp/msa21641.2{*}   January 20, 2003 03:59  ..

                             1                                                   50
       msa21641.2{206_090}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
    msa21641.2{206_1169NT}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
    msa21641.2{206_18RS21}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_2603}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_A909}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_H36B}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
 msa21641.2{206_JM9130013}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_COH1}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_M732}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
      msa21641.2{206_M781}   tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
    msa21641.2{206_CJB110}   ~NTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLKPI IDVSGWQLPK
                 Consensus   -********* ********** ********** ********** **********

                             51                                                 100
       msa21641.2{206_090}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
    msa21641.2{206_1169NT}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
    msa21641.2{206_18RS21}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_2603}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_A909}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_H36B}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
 msa21641.2{206_JM9130013}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_COH1}   EIDYDTLSKN ISGVVIRiFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_M732}   EIDYDTLSKN ISGVVIRiFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
      msa21641.2{206_M781}   EIDYDTLSKN ISGVVIRiFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
    msa21641.2{206_CJB110}   EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTTGIDKSF KTHIKEFQKR
                 Consensus   ********** *******_** ********** ********** **********

                             101                                                150
       msa21641.2{206_090}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
    msa21641.2{206_1169NT}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
    msa21641.2{206_18RS21}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_2603}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_A909}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_H36B}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
 msa21641.2{206_JM9130013}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_COH1}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_M732}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
      msa21641.2{206_M781}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
    msa21641.2{206_CJB110}   NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
                 Consensus   ********** ********** ********** ********** **********

                             151                                                200
       msa21641.2{206_090}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
    msa21641.2{206_1169NT}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
    msa21641.2{206_18RS21}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_2603}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_A909}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_H36B}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
 msa21641.2{206_JM9130013}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_COH1}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_M732}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
      msa21641.2{206_M781}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
    msa21641.2{206_CJB110}   KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGFDAV WIPTYGSDSG
                 Consensus   ********** ********** ********** ********** **********
```

Table 53: Comparative Sequences relating to SAG 0755

```
                              201                                                    250
       msa21641.2{206_090}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
    msa21641.2{206_1169NT}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
    msa21641.2{206_18RS21}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_2603}    YYEAAPQTEL KYDLHQYTSQ GYLPGxNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_A909}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_H36B}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
  msa21641.2{206_JM9130013}   YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_COH1}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_M732}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
      msa21641.2{206_M781}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQIaVNKD KKKTYEKLFG
    msa21641.2{206_CJB110}    YYEAAPQTEL KYDLHQYTSQ GYLPGfNQPL DLNQItVNKD KKKTYEKLFG
                 Consensus    ********** ********** *****-**** *****-**** **********

                              251
       msa21641.2{206_090}    KVKE
    msa21641.2{206_1169NT}    KVKE
    msa21641.2{206_18RS21}    KVKE
      msa21641.2{206_2603}    KVKE
      msa21641.2{206_A909}    KVKE
      msa21641.2{206_H36B}    KVKE
  msa21641.2{206_JM9130013}   KVKE
      msa21641.2{206_COH1}    KVKE
      msa21641.2{206_M732}    KVKE
      msa21641.2{206_M781}    KVKE
    msa21641.2{206_CJB110}    KVKE
                 Consensus    ****
```

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5401
STRAIN 2603
TTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTT
ATGATTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATAATTGG
GAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAATACTTTTGTTCCTATG
GGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGCTAATGCTGTT
TTTAAAGAATACGGTATTTCAGTGAAATGGCAGCCTATTAACTGGGATATGAAAGAAACT
GAACTTAATAATGGTAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGT
GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAA
ACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
GGTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA
GGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTTTGATTGATTTAAAAAATAAC
CGTATTGATGGTCTTTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGA
AATATAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGA
GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA
GAA

SEQ ID NO. 5402
STRAIN 090
ATTGGGaACATTATC
AAAAGGAAAAGAAAATTACTATTGGATTTGATAATACTTTTGTTCCTATG
GGATTTGAAAGCCGTTCTGGTGACTAtACCGGCTTTGATATTGATTTAGC
TAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAAATGGCAGCCTATTA
ACTGGGATATGAAAGAAACTGAACTTAATAATGGTAATATAGACCTTATT
TGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC
AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATCAC
ATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
GGTTCATCTGGTTTTGATGCTTTTAATGCTAAACCTGATATTTTAAAAAA
GTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTT
TGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATTGATGAAGTT
TATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTATTT
TGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGAGCTCGCAAAG
TTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
AATAAGGGAAAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
TTATAGTAAAGAA

SEQ ID NO. 5403
STRAIN A909
ATTGGG
aACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAATACTTTT
GTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATAT
TGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAAATGGC
AGCCTATTAACTGGGATAtgAAAGAAACTGAACTTAATAATGGTAATATA
GACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT
CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAA
CTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGA
GCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATAT
TTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGtTCAATACGATACTTTCA
CTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATT
GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGC
TTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGAG
CTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAA
CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG
TGAAGATGTTTATAGTAAAGaA

SEQ ID NO. 5404
STRAIN H36B
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATT
TGATAATACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATA
CCGGCTTTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATT
TCAGTGAAATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTTAA
TAATGGTAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAAC
GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA
ATTGTTACTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGG
GAAAAAACTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACG
CTAAACCTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGtTCAA
TACGATACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGA
TGGTCTTTTGATTGATGAAGTtTATGCTAACTATTATTTAAAGCAAGAAG
GAAATATAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAgAAAAT
TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAA
CAAAGCTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT
ACAAATGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5405
STRAIN 18RS21
ATTGGGAACATTA
TCAAAAGGAAAAGAAAATTACTATTGGATTTGATAATACTTTTGTTCCTA
TGGGATTTGAAAGTCGTTCTGGTGACTAtACCGGCTTTGATATTGATTTA
GCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAAATGGCAGCCTAT
TAACTGGGATATGAAAGAAACTGAACTTAATAATGGTAATATAGACCTTA
TTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTT
ACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATC

Table 54: Comparative Sequences relating to SAG0949

ACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGT
CGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATATTTTAAAA
AAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGC
TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATTGATGAAG
TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTAT
TTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGAGCTCGTAA
AGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTC
ATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGAT
GTTTATAGTAAAGAA

SEQ ID NO. 5406
STRAIN M732
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTTAATAATGG
TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
ACTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAAC
CTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTA
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5407
STRAIN COH1
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTTAATAATGG
TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
ACTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAAC
CTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTA
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5408
STRAIN M781
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATA
ATACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGC
TTTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGT
GAAATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTTAATAATG
GTAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCT
AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGT
TACTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAA
AACTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAA
CCTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGA
TACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTC
TTTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAAT
ATAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGT
AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAG
CTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAA
TGGTTTGGTGAAGATGTTTATAGTAAAGaA

SEQ ID NO. 5409
STRAIN CJB110
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAAT
ACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTT
TGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGA
AATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTTAATAATGGT
AATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAA
AAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTA
CTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAA
CTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAACGCTAAACC
TGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATA
CTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTT
TTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATAT
AAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAG
TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCT
TTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATG
GTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5410

Table 54: Comparative Sequences relating to SAG0949

```
STRAIN 1169NT
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAAACTGAACTCAATAATGG
TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAA
ACTAGGAGCCCAGTCGGGTTCATCTGGTTTTGATGCTTTTAATGCTAAAC
CTGACATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTTAAAACTGCTTATCAAGGAGAAAATTTTGTA
GTAGGAGCTCGCAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAAATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA
```

SEQ ID NO. 5411

```
STRAIN JM9130013
ATTGGGAACATTATC
AAAAGGAAAAGAAAATTACTATTGGATTTGATAATACTTTTGTTCCTATG
GGATTTGAAAGTCGTTCTGGTGACTAtACCGGCTTTGATATTGATTTAGC
TAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAAATGGCAGCCTATTA
ACTGGGATATGAAAGAAACTGAACTTAATAATGGTAATATAGACCTTATT
TGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC
AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATCAC
ATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
GGTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATATTTTAAAAAA
GTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGCTT
TGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATTGATGAAGTT
TATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTATTT
TGTTAAAACTGCTTATCAAGGAGAAAATTTTGTAGTAGGAGCTCGTAAAG
TTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
TTATAGTAAAGAA
```

```
PRETTY of: /biotmp/msa39314.2{*}   February 18, 2003 11:01  ..

                           1                                                      50
  msa39314.2{225_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_2603}   ttgactcaca aaaatatatt attaaccatt atatttggat tatttatgat
    msa39314.2{225_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa39314.2{225_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa39314.2{225_KM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa39314.2{225_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa39314.2{225_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus   ********** ********** ********** ********** **********

                           51                                                    100
  msa39314.2{225_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_2603}   tatattatca gcatgtggta tgtctaataa ggaaatggct ggtattgata
    msa39314.2{225_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa39314.2{225_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa39314.2{225_KM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa39314.2{225_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa39314.2{225_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa39314.2{225_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus   ********** ********** ********** ********** **********

                           101                                                   150
  msa39314.2{225_18RS21}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_2603}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_A909}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
  msa39314.2{225_CJB110}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_COH1}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_H36B}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
msa39314.2{225_KM9130013}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_M732}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
    msa39314.2{225_M781}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
     msa39314.2{225_090}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
  msa39314.2{225_1169NT}   ATTGGGAACA TTATCAAAAG GAAAAGAAAA TTACTATTGG ATTTGATAAT
               Consensus   ********** ********** ********** ********** **********

                           151                                                   200
  msa39314.2{225_18RS21}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
    msa39314.2{225_2603}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
```

Table 54: Comparative Sequences relating to SAG0949

```
   msa39314.2{225_A909}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
  msa39314.2{225_CJB110}  ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
   msa39314.2{225_COH1}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
   msa39314.2{225_H36B}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
msa39314.2{225_KM9130013} ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
   msa39314.2{225_M732}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
   msa39314.2{225_M781}   ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
    msa39314.2{225_090}   ACTTTTGTTC CTATGGGATT TGAAAGcCGT TCTGGTGACT ATACCGGCTT
  msa39314.2{225_1169NT}  ACTTTTGTTC CTATGGGATT TGAAAGtCGT TCTGGTGACT ATACCGGCTT
               Consensus  ********** ********** ******_*** ********** **********

                          201                                                250
  msa39314.2{225_18RS21}  TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_2603}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_A909}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
  msa39314.2{225_CJB110}  TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_COH1}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_H36B}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
msa39314.2{225_KM9130013} TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_M732}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
   msa39314.2{225_M781}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
    msa39314.2{225_090}   TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
  msa39314.2{225_1169NT}  TGATATTGAT TTAGCTAATG CTGTTTTTAA AGAATACGGT ATTTCAGTGA
               Consensus  ********** ********** ********** ********** **********

                          251                                                300
  msa39314.2{225_18RS21}  AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_2603}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_A909}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
  msa39314.2{225_CJB110}  AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_COH1}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_H36B}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
msa39314.2{225_KM9130013} AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_M732}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
   msa39314.2{225_M781}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
    msa39314.2{225_090}   AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT tAATAATGGT
  msa39314.2{225_1169NT}  AATGGCAGCC TATTAACTGG GATATGAAAG AAACTGAACT cAATAATGGT
               Consensus  ********** ********** ********** ********** _*********

                          301                                                350
  msa39314.2{225_18RS21}  AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_2603}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_A909}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
  msa39314.2{225_CJB110}  AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_COH1}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_H36B}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
msa39314.2{225_KM9130013} AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_M732}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
   msa39314.2{225_M781}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
    msa39314.2{225_090}   AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
  msa39314.2{225_1169NT}  AATATAGACC TTATTTGGAA TGGTTATTCA AAAACGGCAG AACGTGCTAA
               Consensus  ********** ********** ********** ********** **********

                          351                                                400
  msa39314.2{225_18RS21}  AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_2603}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_A909}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
  msa39314.2{225_CJB110}  AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_COH1}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_H36B}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
msa39314.2{225_KM9130013} AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_M732}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
   msa39314.2{225_M781}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
    msa39314.2{225_090}   AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
  msa39314.2{225_1169NT}  AAAAGTCGCT TTTACAAACC CATATATGAA TAATCATCAA GTAATTGTTA
               Consensus  ********** ********** ********** ********** **********

                          401                                                450
  msa39314.2{225_18RS21}  CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_2603}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_A909}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
  msa39314.2{225_CJB110}  CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_COH1}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_H36B}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
msa39314.2{225_KM9130013} CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_M732}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
   msa39314.2{225_M781}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
    msa39314.2{225_090}   CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
  msa39314.2{225_1169NT}  CTAAAACTTC ATCACATATT AATAGTATTA AGGATATGAA GGGGAAAAAA
               Consensus  ********** ********** ********** ********** **********

                          451                                                500
  msa39314.2{225_18RS21}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
```

Table 54: Comparative Sequences relating to SAG0949

```
        msa39314.2{225_2603}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
        msa39314.2{225_A909}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
      msa39314.2{225_CJB110}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
        msa39314.2{225_COH1}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
        msa39314.2{225_H36B}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
  msa39314.2{225_KM9130013}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
        msa39314.2{225_M732}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
        msa39314.2{225_M781}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AcGCTAAACC
         msa39314.2{225_090}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AtGCTAAACC
     msa39314.2{225_1169NT}  CTAGGAGCCC AGTCGGGTTC ATCTGGTTTT GATGCTTTTA AtGCTAAACC
                  Consensus  ********** ********** ********** ********** *-********

                             501                                              550
      msa39314.2{225_18RS21}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_2603}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_A909}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
      msa39314.2{225_CJB110}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_COH1}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_H36B}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
  msa39314.2{225_KM9130013}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_M732}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
        msa39314.2{225_M781}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
         msa39314.2{225_090}  TGAtATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
     msa39314.2{225_1169NT}  TGAcATTTTA AAAAAGTTTG TAAAAGGAAA AGAAGCAGTT CAATACGATA
                  Consensus  ***-****** ********** ********** ********** **********

                             551                                              600
      msa39314.2{225_18RS21}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_2603}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_A909}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
      msa39314.2{225_CJB110}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_COH1}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_H36B}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
  msa39314.2{225_KM9130013}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_M732}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
        msa39314.2{225_M781}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
         msa39314.2{225_090}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
     msa39314.2{225_1169NT}  CTTTCACTCA GGCTTTGATT GATTTAAAAA ATAACCGTAT TGATGGTCTT
                  Consensus  ********** ********** ********** ********** **********

                             601                                              650
      msa39314.2{225_18RS21}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_2603}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_A909}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
      msa39314.2{225_CJB110}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_COH1}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_H36B}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
  msa39314.2{225_KM9130013}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_M732}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
        msa39314.2{225_M781}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
         msa39314.2{225_090}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
     msa39314.2{225_1169NT}  TTGATTGATG AAGTTTATGC TAACTATTAT TTAAAGCAAG AAGGAAATAT
                  Consensus  ********** ********** ********** ********** **********

                             651                                              700
      msa39314.2{225_18RS21}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_2603}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_A909}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
      msa39314.2{225_CJB110}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_COH1}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_H36B}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
  msa39314.2{225_KM9130013}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_M732}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
        msa39314.2{225_M781}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
         msa39314.2{225_090}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
     msa39314.2{225_1169NT}  AAAAGCTTAT TATTTTGTTA AAACTGCTTA TCAAGGAGAA AATTTTGTAG
                  Consensus  ********** ********** ********** ********** **********

                             701                                              750
      msa39314.2{225_18RS21}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_2603}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_A909}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
      msa39314.2{225_CJB110}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_COH1}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_H36B}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
  msa39314.2{225_KM9130013}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_M732}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
        msa39314.2{225_M781}  TAGGAGCTCG tAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
         msa39314.2{225_090}  TAGGAGCTCG cAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
     msa39314.2{225_1169NT}  TAGGAGCTCG cAAAGTTGAT CGTAGACTAA TTGAAAAGAT TAACAAAGCT
                  Consensus  ********** -********* ********** ********** **********

                             751                                              800
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Table 54: Comparative Sequences relating to SAG0949

```
  msa39314.2{225_18RS21}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_2603}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_A909}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
  msa39314.2{225_CJB110}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_COH1}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_H36B}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
msa39314.2{225_KM9130013}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_M732}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
    msa39314.2{225_M781}  TTCAAACAGC TTCATAATAA GGGgAgATTT CAAAAAATCT CTTACAAATG
     msa39314.2{225_090}  TTCAAACAGC TTCATAATAA GGGaAaATTT CAAAAAATCT CTTACAAATG
  msa39314.2{225_1169NT}  TTCAAACAGC TTCATAATAA GGGgAaATTT CAAAAAATCT CTTACAAATG
               Consensus  ********** ********** ***-*-**** ********** **********

                          801                        828
  msa39314.2{225_18RS21}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_2603}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_A909}  GTTTGGTGAA GATGTTTATA GTAAAGAA
  msa39314.2{225_CJB110}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_COH1}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_H36B}  GTTTGGTGAA GATGTTTATA GTAAAGAA
msa39314.2{225_KM9130013}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_M732}  GTTTGGTGAA GATGTTTATA GTAAAGAA
    msa39314.2{225_M781}  GTTTGGTGAA GATGTTTATA GTAAAGAA
     msa39314.2{225_090}  GTTTGGTGAA GATGTTTATA GTAAAGAA
  msa39314.2{225_1169NT}  GTTTGGTGAA GATGTTTATA GTAAAGAA
               Consensus  ********** ********** ********
```

SEQ ID NO. 5412
STRAIN 2603 frame: 1
LTHKNILLTIIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR
SGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETELNNGNIDLIWNGYSKTAERAKKVA
FTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQSGSSGFDAFNAKPDILKKFVKGKEAV
QYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQEGNIKAYYFVKTAYQGENFVVGARKVD
RRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYSKE

SEQ ID NO. 5413
STRAIN 090 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGKFQKISYKWFGEDVYS
KE

SEQ ID NO. 5414
STRAIN A909 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5415
STRAIN H36B frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5416
STRAIN 18RS21 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5417
STRAIN M732 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5418
STRAIN COH1 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5419
STRAIN M781 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5420
STRAIN CJB110 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

SEQ ID NO. 5421
STRAIN 1169NT frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGKFQKISYKWFGEDVYS
KE

SEQ ID NO. 5422
STRAIN JM9130013 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYYLKQE
GNIKAYYFVKTAYQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDVYS
KE

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PRETTY of: /biotmp/msa45901.2{*}    February 19, 2003 03:09  ..

                                1                                                    50
       msa45901.2{225_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
    msa45901.2{225_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
    msa45901.2{225_18RS21}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
      msa45901.2{225_2603}    lthknillti ifglfmiils acgmsnkema gidnWEHYQK EKKITIGFDN
      msa45901.2{225_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
    msa45901.2{225_CJB110}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
      msa45901.2{225_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
      msa45901.2{225_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
 msa45901.2{225_JM9130013}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
      msa45901.2{225_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
      msa45901.2{225_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~WEHYQK EKKITIGFDN
                 Consensus    ********** ********** ********** ********** **********

                              51                                                  100
       msa45901.2{225_090}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
    msa45901.2{225_1169NT}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
    msa45901.2{225_18RS21}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_2603}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_A909}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
    msa45901.2{225_CJB110}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_COH1}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_H36B}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
 msa45901.2{225_JM9130013}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_M732}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
      msa45901.2{225_M781}    TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
                 Consensus    ********** ********** ********** ********** **********

                              101                                                 150
       msa45901.2{225_090}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
    msa45901.2{225_1169NT}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
    msa45901.2{225_18RS21}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_2603}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_A909}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
    msa45901.2{225_CJB110}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_COH1}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_H36B}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
 msa45901.2{225_JM9130013}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_M732}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
      msa45901.2{225_M781}    NIDLIWNGYS KTAERAKKVA FTNPYMNNHQ VIVTKTSSHI NSIKDMKGKK
                 Consensus    ********** ********** ********** ********** **********

                              151                                                 200
       msa45901.2{225_090}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
    msa45901.2{225_1169NT}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
    msa45901.2{225_18RS21}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
      msa45901.2{225_2603}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
      msa45901.2{225_A909}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
    msa45901.2{225_CJB110}    LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
```

Table 54: Comparative Sequences relating to SAG0949

```
      msa45901.2{225_COH1}  LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
      msa45901.2{225_H36B}  LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
 msa45901.2{225_JM9130013}  LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
      msa45901.2{225_M732}  LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
      msa45901.2{225_M781}  LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDTFTQALI DLKNNRIDGL
                 Consensus  ********** ********** ********** ********** **********

                            201                                              250
       msa45901.2{225_090}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
    msa45901.2{225_1169NT}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
    msa45901.2{225_18RS21}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_2603}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_A909}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
    msa45901.2{225_CJB110}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_COH1}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_H36B}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
 msa45901.2{225_JM9130013}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_M732}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
      msa45901.2{225_M781}  LIDEVYANYY LKQEGNIKAY YFVKTAYQGE NFVVGARKVD RRLIEKINKA
                 Consensus  ********** ********** ********** ********** **********

                            251                    276
       msa45901.2{225_090}  FKQLHNKGkF QKISYKWFGE DVYSKE
    msa45901.2{225_1169NT}  FKQLHNKGkF QKISYKWFGE DVYSKE
    msa45901.2{225_18RS21}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_2603}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_A909}  FKQLHNKGrF QKISYKWFGE DVYSKE
    msa45901.2{225_CJB110}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_COH1}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_H36B}  FKQLHNKGrF QKISYKWFGE DVYSKE
 msa45901.2{225_JM9130013}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_M732}  FKQLHNKGrF QKISYKWFGE DVYSKE
      msa45901.2{225_M781}  FKQLHNKGrF QKISYKWFGE DVYSKE
                 Consensus  ********_* ********** ******
```

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501
STRAIN 2603
ATGCTTAAATCTTTTTTGATTTTCTTAGTTCGCTTTTACCAAAAAAATATTTCTCCAGCT
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTATTTTGCGATGTCATCCCTTA
GCCCACGGAGGAAATGATCCTGTCCCTGATCATTTTAGCTTAAGACGTAATAAAACGGAT
ATATCAGAT

SEQ ID NO. 5502
STRAIN 090
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTT

SEQ ID NO. 5503
STRAIN A909
TTCCCAGCTAGCTGTCGTTATCGTCCAACtTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAgCTTAAGACGTAATAAAACGGATATA

SEQ ID NO. 5504
STRAIN H36B
TTCCCAGCTAGCTGTCGTTATCGTCCaACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTTCTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5505
STRAIN 18RS21
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5506
STRAIN M732
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAgCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5507
STRAIN COH1
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTATTTTGCGATGTCATCCCTTA
GCCCACGGAGGAAATGAtCCTGtCCCTGATCATTTTAGCT

SEQ ID NO. 5508
STRAIN M781
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5509
STRAIN CJB110
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5510
STRAIN 1169NT
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
TATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5511
STRAIN JM9130013
TTCCCAGCTAGCTGTCGTTATCGTCCAACTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTTCTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

```
PRETTY of: /biotmp/msa119306.2{*}   April 29, 2003 06:23  ..

                                1                                                   50
      msa119306.2{233_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa119306.2{233_JM9130013}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

Table 55: Comparative Sequences relating to SAG1592

```
          msa119306.2{233_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa119306.2{233_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa119306.2{233_2603}  atgcttaaat ctttttttgat tttcttagtt cgcttttacc aaaaaaatat
         msa119306.2{233_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa119306.2{233_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa119306.2{233_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa119306.2{233_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa119306.2{233_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa119306.2{233_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                     Consensus  ********** ********** ********** ********** **********

                                51                                                100
         msa119306.2{233_H36B}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
    msa119306.2{233_JM9130013}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
          msa119306.2{233_090}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
       msa119306.2{233_18RS21}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
         msa119306.2{233_2603}  ttctccagct TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
         msa119306.2{233_A909}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
       msa119306.2{233_CJB110}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
         msa119306.2{233_COH1}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
         msa119306.2{233_M732}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
         msa119306.2{233_M781}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
       msa119306.2{233_1169NT}  ~~~~~~~~~~ TTCCCAGCTA GCTGTCGTTA TCGTCCAACT TGCTCTACGT
                     Consensus  ********** ********** ********** ********** **********

                                101                                               150
         msa119306.2{233_H36B}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT tcTGATGGGG
    msa119306.2{233_JM9130013}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT tcTGATGGGG
          msa119306.2{233_090}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
       msa119306.2{233_18RS21}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
         msa119306.2{233_2603}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
         msa119306.2{233_A909}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
       msa119306.2{233_CJB110}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
         msa119306.2{233_COH1}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
         msa119306.2{233_M732}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
         msa119306.2{233_M781}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT gtTGATGGGG
       msa119306.2{233_1169NT}  ATATGATAGA AGCTATTCAA AAACATGGTC TAAAAGGTGT ggTGATGGGG
                     Consensus  ********** ********** ********** ********** --********

                                151                                               200
         msa119306.2{233_H36B}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
    msa119306.2{233_JM9130013}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
          msa119306.2{233_090}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
       msa119306.2{233_18RS21}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
         msa119306.2{233_2603}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
         msa119306.2{233_A909}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
       msa119306.2{233_CJB110}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
         msa119306.2{233_COH1}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
         msa119306.2{233_M732}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
         msa119306.2{233_M781}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
       msa119306.2{233_1169NT}  ATTGCACGTA TTTTGCGATG TCATCCCTTA GCCCACGGAG GAAATGATCC
                     Consensus  ********** ********** ********** ********** **********

                                201                                              249
         msa119306.2{233_H36B}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
    msa119306.2{233_JM9130013}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
          msa119306.2{233_090}  TGTCCCTGAT cATTTTAGCT t~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
       msa119306.2{233_18RS21}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
         msa119306.2{233_2603}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
         msa119306.2{233_A909}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat ata~~~~~~
       msa119306.2{233_CJB110}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
         msa119306.2{233_COH1}  TGTCCCTGAT cATTTTAGCT ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
         msa119306.2{233_M732}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
         msa119306.2{233_M781}  TGTCCCTGAT cATTTTAGCT taagacgtaa taaaacggat atatcagat
       msa119306.2{233_1169NT}  TGTCCCTGAT tATTTTAGCT taagacgtaa taaaacggat atatcagat
                     Consensus  ********** -********* ---------- ---------- ---------
```

SEQ ID NO. 5512
STRAIN 2603 frame: 1
MLKSFLIFLVRFYQKNISPAFPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPL
AHGGNDPVPDHFSLRRNKTDISD

SEQ ID NO. 5513
STRAIN 090 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFS

SEQ ID NO. 5514
STRAIN A909 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
I

SEQ ID NO. 5515
STRAIN H36B frame: 1

Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5516
STRAIN 18RS21 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5517
STRAIN M732 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5518
STRAIN COH1 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFS

SEQ ID NO. 5519
STRAIN M781 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5520
STRAIN CJB110 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5521
STRAIN 1169NT frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVVMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD
ISD

SEQ ID NO. 5522
STRAIN JM9130013 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

```
PRETTY of: /biotmp/msa119415.2{*}   April 29, 2003 06:25  ..

                                   1                                                    50
        msa119415.2{233_090}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
      msa119415.2{233_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_A909}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_2603}  mlksfliflv rfyqknispa FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
      msa119415.2{233_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
   msa119415.2{233_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_M732}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
        msa119415.2{233_M781}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVlMG
      msa119415.2{233_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ FPASCRYRPT CSTYMIEAIQ KHGLKGVvMG
                   Consensus  ********** ********** ********** ********** *******_**

                                   51                              83
        msa119415.2{233_090}  IARILRCHPL AHGGNDPVPD hFS~~~~~~~ ~~~
      msa119415.2{233_18RS21}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
        msa119415.2{233_COH1}  IARILRCHPL AHGGNDPVPD hFS~~~~~~~ ~~~
        msa119415.2{233_A909}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD I~~
        msa119415.2{233_2603}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
      msa119415.2{233_CJB110}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
        msa119415.2{233_H36B}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
   msa119415.2{233_JM9130013}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
        msa119415.2{233_M732}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
        msa119415.2{233_M781}  IARILRCHPL AHGGNDPVPD hFSLRRNKTD ISD
      msa119415.2{233_1169NT}  IARILRCHPL AHGGNDPVPD yFSLRRNKTD ISD
                   Consensus  ********** ********** _********* ***
```

Table 56: Comparative Sequences relating to SAG0806

SEQ ID NO. 5601
STRAIN 2603
aagaagcttacttttatttgggatttagatgggacattaatagattcgta
tgtaccaattatggaagctcttgaagaaacctatcgtcattttggtttaa
tatttgataaagaattaatccatgaatatatttacaggaatcagtgggg
aaattattggtaaacctttcagaggaagagcaaatacctcatgaaaaact
gaaagcatattttacaaaagaacaagaaagtcgagattctaaaatacatt
taatgccatatgcaaaagagattttagaatggaccaaagaacaagatatc
cccaattttatgtatacacataaaggagcaagtacgcattcagtgttgga
aaccttgcagatctctcattattttgatgaaattttaactggtgtttcgg
gattcgagcgaaaaccacatccacaagggattaattatttagttaaacga
tattctttagataaatcaatgacttattacataggagatcgtccactaga
tttggaggttgctcaaaatgctggtataaaatccataaacttaaggttag
agaattccaaagaaaactataatatttcaagtctcaaagatataatatca
cttgatttcactcgtttggat

SEQ ID NO. 5602
STRAIN COH1
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAA
TAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCAT
TTTGGCTTAATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGA
ATCAGTGGGGCAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTC
ATGAAAAACTGAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCT
AAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGA
ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
CAGTGTTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACT
GGTGTTTCGGGATTCGAGCGAAAACCACATCCACAAGGGATTAATTATTT
AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC
GTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAAC
TTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCTCAAAGA
TATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5603
STRAIN A909
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAAT
AGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAT
ATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTGGT
AAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
ACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATG
GACCAAAGAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTC
AGTGTTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGG
ATTCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGA
TAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGC
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAG
TCTCAAAGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5604
STRAIN H36B
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCG
TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAATATTTGAT
AAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTGGTAAACCTT
TCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACAAGAA
AGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAA
GAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTGTTG
GAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGGATTCGAG
CGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAAATCA
ATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATA
AAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCTCAAA
GATATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5605
STRAIN 18RS21
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATT
CGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAATATTTG
ATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTGGTAAACC
TTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACAAG
AAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGACCA
AAGAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTGT
TGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGGATTCG
AGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAAAT
CAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTA
TAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCTCA
AAGATATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5606
STRAIN M732
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGAT
TCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAATATTT
GATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATTGGTAAAC
CTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACAA
GAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGACC
AAAGAACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTG

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGGATTC
GAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAAA
TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGT
ATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCTC
AAAGATATAATATCACTTGATTTCACTCGTTTGGAT

SEQ ID NO. 5607
STRAIN CJB110
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT
AATAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT
AATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATT
GGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAA
AGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGA
ATGGACCAAAGAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA
TTCAGTGTTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTC
TGGATTCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTT
AGATAAATCAATGACTTATTACATAGGAGATCGTCCCCTAGATTTGGAGGTTGCTCAAAA
TGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTC
AAGTCTCAAGGATATAATATCACTTGATTTCACTCGTT

SEQ ID NO. 5608
STRAIN 1169NT
aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGTATGTACCAATTA
TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAATCC
ATGAATATATTTTACAGGAATCAGTGGGGAAATTATTGGTAAACCTTTCAGAGGAAGAGC
AAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTA
AAATACATTTAATGCCATACGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATATCC
CCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTGTTGGAAACCTTGCAGA
TCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGGATTCGAGCGAAAACCACATC
CACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACA
TAGGAGATCGTCCCCTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAACT
TAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCTCAAGGATATAATATCAC
TTGATTTCACTCGTTTGGAT

SEQ ID NO. 5609
STRAIN JM9130013
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA
TTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAATATT
TGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTGGTAAA
CCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACA
AGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGAATGGAC
CAAAGAACAAGATATCCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGT
GTTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCGGGATT
CGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAA
ATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGG
TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATAATATTTCAAGTCT
CAAAGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5610
STRAIN 090
AAGAAGCTTACTTTTATTTGG
GATTTAGATGGGACATTAATAGATTCGTATGTACCAATTATGGAAGCTCT
TGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAATCC
ATGAATATATTTTACAGGAATCAGTGGGGCAATTATTGGTAAACCTTTCA
GAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
ACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGA
TTTTAGAATGGACCAAAGAACAAGATATCCCCAATTTTATGTATACACAT
AAAGGAGCAAGTACGCATTCAGTGTTGGAAACCTTGCAGATCTCTCATTA
TTTTGATGAAATTTTAACTGGTGTTTCTGGATTCGAGCGAAAACCACATC
CACAAGGGATTAATTATTTAGTTAAACGATATTCTTTAGATAAATCAATG
ACTTATTACATAGGAGATCGTCCCCTAGATTTGGAGGTTGCTCAAAATGC
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACTATA
ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5611
STRAIN M781
AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGT
ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA
ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGG
GCAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAAC
TGAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTyTAAAATACAT
TTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATAT
TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTGTTGG
AAACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTTCG
GGATTCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACG
ATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG
ATTTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTA
GAGAATTCCAAAGAAAACTATAATATTTCAAGTCTCAAAGATATAATATC
ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2{*}   January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

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                           1                                                   50
   msa45163.2{240_18RS21}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_2603}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_A909}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_H36B}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
msa45163.2{240_JM9130013}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_COH1}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_M732}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
     msa45163.2{240_M781}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
      msa45163.2{240_090}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
   msa45163.2{240_CJB110}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
   msa45163.2{240_1169NT}  AAGAAGCTTA CTTTTATTTG GGATTTAGAT GGGACATTAA TAGATTCGTA
                Consensus  ********** ********** ********** ********** **********

                           51                                                 100
   msa45163.2{240_18RS21}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGtTTAA
     msa45163.2{240_2603}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGtTTAA
     msa45163.2{240_A909}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGtTTAA
     msa45163.2{240_H36B}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGtTTAA
msa45163.2{240_JM9130013}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGtTTAA
     msa45163.2{240_COH1}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
     msa45163.2{240_M732}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
     msa45163.2{240_M781}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
      msa45163.2{240_090}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
   msa45163.2{240_CJB110}  TGTACCAATT ATgGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
   msa45163.2{240_1169NT}  TGTACCAATT ATaGAAGCTC TTGAAGAAAC CTATCGTCAT TTTGGcTTAA
                Consensus  ********** **_******* ********** ********** *****_****

                           101                                                150
   msa45163.2{240_18RS21}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_2603}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_A909}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_H36B}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
msa45163.2{240_JM9130013}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_COH1}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_M732}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
     msa45163.2{240_M781}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
      msa45163.2{240_090}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
   msa45163.2{240_CJB110}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
   msa45163.2{240_1169NT}  TATTTGATAA AGAATTAATC CATGAATATA TTTTACAGGA ATCAGTGGGG
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
   msa45163.2{240_18RS21}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_2603}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_A909}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_H36B}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
msa45163.2{240_JM9130013}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_COH1}  cAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_M732}  cAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
     msa45163.2{240_M781}  cAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
      msa45163.2{240_090}  cAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
   msa45163.2{240_CJB110}  cAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
   msa45163.2{240_1169NT}  aAATTATTGG TAAACCTTTC AGAGGAAGAG CAAATACCTC ATGAAAAACT
                Consensus  -********* ********** ********** ********** **********

                           201                                                250
   msa45163.2{240_18RS21}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_2603}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_A909}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_H36B}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
msa45163.2{240_JM9130013}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_COH1}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_M732}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
     msa45163.2{240_M781}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTyT AAAATACATT
      msa45163.2{240_090}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
   msa45163.2{240_CJB110}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
   msa45163.2{240_1169NT}  GAAAGCATAT TTTACAAAAG AACAAGAAAG TCGAGATTcT AAAATACATT
                Consensus  ********** ********** ********** ********_* **********

                           251                                                300
   msa45163.2{240_18RS21}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
     msa45163.2{240_2603}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
     msa45163.2{240_A909}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
     msa45163.2{240_H36B}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
msa45163.2{240_JM9130013}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
     msa45163.2{240_COH1}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATt
     msa45163.2{240_M732}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATt
     msa45163.2{240_M781}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATt
      msa45163.2{240_090}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
   msa45163.2{240_CJB110}  TAATGCCATA tGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
   msa45163.2{240_1169NT}  TAATGCCATA cGCAAAAGAG ATTTTAGAAT GGACCAAAGA ACAAGATATc
                Consensus  ********** -********* ********** ********** *********-
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Table 56: Comparative Sequences relating to SAG0806

```
                               301                                                    350
    msa45163.2{240_18RS21}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_2603}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_A909}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_H36B}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
msa45163.2{240_JM9130013}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_COH1}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_M732}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
      msa45163.2{240_M781}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
       msa45163.2{240_090}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
    msa45163.2{240_CJB110}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
   msa45163.2{240_1169NT}     CCCAATTTTA TGTATACACA TAAAGGAGCA AGTACGCATT CAGTGTTGGA
                Consensus     ********** ********** ********** ********** **********

                               351                                                    400
    msa45163.2{240_18RS21}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_2603}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_A909}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_H36B}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
msa45163.2{240_JM9130013}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_COH1}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_M732}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
      msa45163.2{240_M781}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
       msa45163.2{240_090}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCtG
    msa45163.2{240_CJB110}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCtG
   msa45163.2{240_1169NT}     AACCTTGCAG ATCTCTCATT ATTTTGATGA AATTTTAACT GGTGTTTCgG
                Consensus     ********** ********** ********** ********** ********-*

                               401                                                    450
    msa45163.2{240_18RS21}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_2603}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_A909}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_H36B}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
msa45163.2{240_JM9130013}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_COH1}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_M732}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
      msa45163.2{240_M781}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
       msa45163.2{240_090}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
    msa45163.2{240_CJB110}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
   msa45163.2{240_1169NT}     GATTCGAGCG AAAACCACAT CCACAAGGGA TTAATTATTT AGTTAAACGA
                Consensus     ********** ********** ********** ********** **********

                               451                                                    500
    msa45163.2{240_18RS21}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_2603}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_A909}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_H36B}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
msa45163.2{240_JM9130013}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_COH1}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_M732}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
      msa45163.2{240_M781}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCaCTAGA
       msa45163.2{240_090}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCcCTAGA
    msa45163.2{240_CJB110}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCcCTAGA
   msa45163.2{240_1169NT}     TATTCTTTAG ATAAATCAAT GACTTATTAC ATAGGAGATC GTCCcCTAGA
                Consensus     ********** ********** ********** ********** ****-*****

                               501                                                    550
    msa45163.2{240_18RS21}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_2603}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_A909}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_H36B}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
msa45163.2{240_JM9130013}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_COH1}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_M732}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
      msa45163.2{240_M781}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
       msa45163.2{240_090}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
    msa45163.2{240_CJB110}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
   msa45163.2{240_1169NT}     TTTGGAGGTT GCTCAAAATG CTGGTATAAA ATCCATAAAC TTAAGGTTAG
                Consensus     ********** ********** ********** ********** **********

                               551                                                    600
    msa45163.2{240_18RS21}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_2603}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_A909}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_H36B}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
msa45163.2{240_JM9130013}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_COH1}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_M732}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
      msa45163.2{240_M781}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAaGA TATAATATCA
       msa45163.2{240_090}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAgGA TATAATATCA
    msa45163.2{240_CJB110}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAgGA TATAATATCA
   msa45163.2{240_1169NT}     AGAATTCCAA AGAAAACTAT AATATTTCAA GTCTCAAgGA TATAATATCA
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Table 56: Comparative Sequences relating to SAG0806

```
               Consensus  ********** ********** ********** *******_** **********

                          601                  621
     msa45163.2{240_18RS21}  CTTGATTTCA CTCGTttgga t
      msa45163.2{240_2603}   CTTGATTTCA CTCGTttgga t
      msa45163.2{240_A909}   CTTGATTTCA CTCGT------ -
      msa45163.2{240_H36B}   CTTGATTTCA CTCGTttgga t
  msa45163.2{240_JM9130013}  CTTGATTTCA CTCGT------ -
      msa45163.2{240_COH1}   CTTGATTTCA CTCGTttgga t
      msa45163.2{240_M732}   CTTGATTTCA CTCGTttgga t
      msa45163.2{240_M781}   CTTGATTTCA CTCGT------ -
       msa45163.2{240_090}   CTTGATTTCA CTCGT------ -
    msa45163.2{240_CJB110}   CTTGATTTCA CTCGTt----- -
    msa45163.2{240_1169NT}   CTTGATTTCA CTCGTttgga t
               Consensus  ********** *****----- -
```

SEQ ID NO. 5612
STRAIN 2603 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5613
STRAIN A909 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5614
STRAIN H36B frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5615
STRAIN 18RS21 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5616
STRAIN M732 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5617
STRAIN COH1 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5618
STRAIN CJB110 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5619
STRAIN 1169NT frame: 1
KKLTFIWDLDGTLIDSYVPIIEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5620
STRAIN JM9130013 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGKLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5621
STRAIN 090 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ

Table 56: Comparative Sequences relating to SAG0806

```
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5622
STRAIN M781 frame: 1
KKLTFIWDLDGTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDXKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLENSKENYNISSLKDIISLDFTR

PRETTY of: /biotmp/msa45645.2{*}   January 21, 2003 06:57  ..

                           1                                                  50
   msa45645.2{240_18RS21}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_A909}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
msa45645.2{240_JM9130013}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_2603}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_H36B}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
      msa45645.2{240_090}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
   msa45645.2{240_CJB110}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_M781}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_COH1}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
     msa45645.2{240_M732}  KKLTFIWDLD GTLIDSYVPI mEALEETYRH FGLIFDKELI HEYILQESVG
   msa45645.2{240_1169NT}  KKLTFIWDLD GTLIDSYVPI iEALEETYRH FGLIFDKELI HEYILQESVG
                Consensus  ********** ********** -********* ********** **********

                           51                                                100
   msa45645.2{240_18RS21}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_A909}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
msa45645.2{240_JM9130013}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_2603}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_H36B}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
      msa45645.2{240_090}  qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
   msa45645.2{240_CJB110}  qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_M781}  qLLVNLSEEE QIPHEKLKAY FTKEQESRDx KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_COH1}  qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
     msa45645.2{240_M732}  qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
   msa45645.2{240_1169NT}  kLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPYAKE ILEWTKEQDI
                Consensus  -********* ********** *********- ********** **********

                           101                                               150
   msa45645.2{240_18RS21}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_A909}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
msa45645.2{240_JM9130013}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_2603}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_H36B}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
      msa45645.2{240_090}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
   msa45645.2{240_CJB110}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_M781}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_COH1}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
     msa45645.2{240_M732}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
   msa45645.2{240_1169NT}  PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLVKR
                Consensus  ********** ********** ********** ********** **********

                           151                                               200
   msa45645.2{240_18RS21}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_A909}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
msa45645.2{240_JM9130013}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_2603}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_H36B}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
      msa45645.2{240_090}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
   msa45645.2{240_CJB110}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_M781}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_COH1}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
     msa45645.2{240_M732}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
   msa45645.2{240_1169NT}  YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLENSKENY NISSLKDIIS
                Consensus  ********** ********** ********** ********** **********

                           201
   msa45645.2{240_18RS21}  LDFTRld
     msa45645.2{240_A909}  LDFTR--
msa45645.2{240_JM9130013}  LDFTR--
     msa45645.2{240_2603}  LDFTRld
     msa45645.2{240_H36B}  LDFTRld
      msa45645.2{240_090}  LDFTR--
   msa45645.2{240_CJB110}  LDFTR--
     msa45645.2{240_M781}  LDFTR--
     msa45645.2{240_COH1}  LDFTRld
     msa45645.2{240_M732}  LDFTRld
   msa45645.2{240_1169NT}  LDFTRld
                Consensus  *****--
```

Table 57: Comparative Sequences relating to SAG 1488

SEQ ID NO: 5701
STRAIN 2603
ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT
GGAAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTTAAAGTCATAGATGCGGAT
CAAGTGGTTCATAAATTGCAAGCTAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGG
TTGGGTCCCGAGATACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATG
ATTTTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCGT
CAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATATTTTTCATGGAT
ATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGATGAGATTTGGTTGGTATTT
GTTGATAAAGAAAAACAATTACAACGATTAATGGCCCGTAACAACTACAGTCGAGAAGAA
GCAGAATTACGACTTTCACACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTT
ATTATTGACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
CGTTTA

SEQ ID NO: 5702
STRAIN 090
AAGTCAACGGTAACAAAAATAATACGAGAATCAG
GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAG
GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTG
CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
CGTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGAT
ATTTTTCGTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
ACACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTA
ATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
CAACGTTTA

SEQ ID NO: 5703
STRAIN A909
AAGTCAACGGTAACAAAAATAATACGAGAATCAG
GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAG
GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTG
CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
CGTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGAT
ATTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
TTAATGGCCCGTaACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
ACACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTG
ACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
CAACGTTTA

SEQ ID NO: 5704
STRAIN H36B
AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTC
GTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATA
TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
TAATGGCCCGtAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTCA
CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTC
AACGTTTA

SEQ ID NO: 5705
STRAIN 18RS21
AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTC
GTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATA
TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
CACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTC
AACGTTTA

SEQ ID NO: 5706
STRAIN M732
AAGTCAACGGTAACAAAAATAATACGAGAATCAGGTT
TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGGT
GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTGA
TGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGCTA
ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCGT
CAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATATT

Table 57: Comparative Sequences relating to SAG 1488

TTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG
ATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATTA
ATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCACA
CCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGACA
ATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
CGTTTA

SEQ ID NO: 5707
STRAIN COH1
AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGCT
AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCG
TCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATAT
TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
GATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATT
AATGGCCCGTaACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCAC
ACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAC
AATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCA
ACGTTTA

SEQ ID NO: 5708
STRAIN M781
AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTC
GTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATA
TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
CACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTC
AACGTTTA

SEQ ID NO: 5709
STRAIN CJB110
AAGTCAACGGTAACAAAAATAATACGAGAA
TCAGGTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGC
TAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGA
TACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATT
TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT
CATTCGTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAG
AGATATTTTTCGTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAA
TGGTTTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACA
ACGATTAATGGCCCGTaACAACTACAGTCGAGAAGAAGCAGAATTACGAC
TTTCACACCAAATGCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATT
ATTAATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGC
TCTTCAACGTTTA

SEQ ID NO: 5710
STRAIN 1169NT
AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGC
TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTC
GTCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATA
TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGAT
TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTC
AACGTTTA

SEQ ID NO: 5711
STRAIN JM9130013
AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTGCT
AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCG
TCAAGAGTTAGCATGTCAGCGCGACCAATTAAAACAAACAGAAGAGATAT
TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
GATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGATT
AATGGCCCGTAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTCAC
ACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAT
AATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCA
ACGTTTA

Table 57: Comparative Sequences relating to SAG 1488

```
PRETTY of: /biotmp/msa221059.2{*}   February 10, 2003 07:07  ..

                            1                                                      50
     msa221059.2{245_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
msa221059.2{245_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
   msa221059.2{245_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
      msa221059.2{245_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
   msa221059.2{245_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
   msa221059.2{245_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
     msa221059.2{245_2603}  atgcttatga caaaaataat aggactgaca ggagggatag cttctggaAA
     msa221059.2{245_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
     msa221059.2{245_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
     msa221059.2{245_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
     msa221059.2{245_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~AA
                 Consensus  ********** ********** ********** ********** **********

                            51                                                    100
     msa221059.2{245_H36B}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
msa221059.2{245_JM9130013}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
   msa221059.2{245_1169NT}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
      msa221059.2{245_090}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
   msa221059.2{245_CJB110}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
   msa221059.2{245_18RS21}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
     msa221059.2{245_2603}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
     msa221059.2{245_A909}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
     msa221059.2{245_COH1}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
     msa221059.2{245_M732}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
     msa221059.2{245_M781}  GTCAACGGTA ACAAAAATAA TACGAGAATC AGGTTTTAAA GTCATAGATG
                 Consensus  ********** ********** ********** ********** **********

                            101                                                   150
     msa221059.2{245_H36B}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
msa221059.2{245_JM9130013}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
   msa221059.2{245_1169NT}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
      msa221059.2{245_090}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
   msa221059.2{245_CJB110}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
   msa221059.2{245_18RS21}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
     msa221059.2{245_2603}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
     msa221059.2{245_A909}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
     msa221059.2{245_COH1}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
     msa221059.2{245_M732}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
     msa221059.2{245_M781}  CGGATCAAGT GGTTCATAAA TTGCAAGCTA AGGGTGGGAA ACTTTACCAA
                 Consensus  ********** ********** ********** ********** **********

                            151                                                   200
     msa221059.2{245_H36B}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
msa221059.2{245_JM9130013}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
   msa221059.2{245_1169NT}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
      msa221059.2{245_090}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
   msa221059.2{245_CJB110}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
   msa221059.2{245_18RS21}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
     msa221059.2{245_2603}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
     msa221059.2{245_A909}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
     msa221059.2{245_COH1}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
     msa221059.2{245_M732}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
     msa221059.2{245_M781}  GCTTTATTAG AATGGTTGGG TCCCGAGATA CTTGATGCTG ATGGTGAGTT
                 Consensus  ********** ********** ********** ********** **********

                            201                                                   250
     msa221059.2{245_H36B}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
msa221059.2{245_JM9130013}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
   msa221059.2{245_1169NT}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
      msa221059.2{245_090}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
   msa221059.2{245_CJB110}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
   msa221059.2{245_18RS21}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
     msa221059.2{245_2603}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
     msa221059.2{245_A909}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
     msa221059.2{245_COH1}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
     msa221059.2{245_M732}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
     msa221059.2{245_M781}  GGATAGACCA AAGCTTTCTC AAATGATTTT TGCTAATCCA GACAATATGA
                 Consensus  ********** ********** ********** ********** **********

                            251                                                   300
     msa221059.2{245_H36B}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
msa221059.2{245_JM9130013}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
   msa221059.2{245_1169NT}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
      msa221059.2{245_090}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
   msa221059.2{245_CJB110}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
   msa221059.2{245_18RS21}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
     msa221059.2{245_2603}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
     msa221059.2{245_A909}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
     msa221059.2{245_COH1}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
     msa221059.2{245_M732}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
```

Table 57: Comparative Sequences relating to SAG 1488

```
     msa221059.2{245_M781}  AGACATCAGC TAGGCTACAA AATAGTATCA TTCGTCAAGA GTTAGCATGT
                 Consensus  ********** ********** ********** ********** **********

                            301                                                350
     msa221059.2{245_H36B}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
 msa221059.2{245_JM9130013} CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
   msa221059.2{245_1169NT}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
      msa221059.2{245_090}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCg TGGATATTCC
   msa221059.2{245_CJB110}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCg TGGATATTCC
   msa221059.2{245_18RS21}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
     msa221059.2{245_2603}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
     msa221059.2{245_A909}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
     msa221059.2{245_COH1}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
     msa221059.2{245_M732}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
     msa221059.2{245_M781}  CAGCGCGACC AATTAAAACA AACAGAAGAG ATATTTTTCa TGGATATTCC
                 Consensus  ********** ********** ********** *********- **********

                            351                                                400
     msa221059.2{245_H36B}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
 msa221059.2{245_JM9130013} TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
   msa221059.2{245_1169NT}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
      msa221059.2{245_090}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
   msa221059.2{245_CJB110}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
   msa221059.2{245_18RS21}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
     msa221059.2{245_2603}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
     msa221059.2{245_A909}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
     msa221059.2{245_COH1}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
     msa221059.2{245_M732}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
     msa221059.2{245_M781}  TTTATTGATT GAAGAAAAGT ATATAAAATG GTTTGATGAG ATTTGGTTGG
                 Consensus  ********** ********** ********** ********** **********

                            401                                                450
     msa221059.2{245_H36B}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
 msa221059.2{245_JM9130013} TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
   msa221059.2{245_1169NT}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
      msa221059.2{245_090}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
   msa221059.2{245_CJB110}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
   msa221059.2{245_18RS21}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
     msa221059.2{245_2603}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
     msa221059.2{245_A909}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
     msa221059.2{245_COH1}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
     msa221059.2{245_M732}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
     msa221059.2{245_M781}  TATTTGTTGA TAAAGAAAAA CAATTACAAC GATTAATGGC CCGTAACAAC
                 Consensus  ********** ********** ********** ********** **********

                            451                                                500
     msa221059.2{245_H36B}  TACAGTCGAG AAGAAGCgGA ATTACGACTT TCACACCAAA TaCCTTTAAC
 msa221059.2{245_JM9130013} TACAGTCGAG AAGAAGCgGA ATTACGACTT TCACACCAAA TaCCTTTAAC
   msa221059.2{245_1169NT}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TaCCTTTAAC
      msa221059.2{245_090}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
   msa221059.2{245_CJB110}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
   msa221059.2{245_18RS21}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
     msa221059.2{245_2603}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
     msa221059.2{245_A909}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
     msa221059.2{245_COH1}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
     msa221059.2{245_M732}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
     msa221059.2{245_M781}  TACAGTCGAG AAGAAGCaGA ATTACGACTT TCACACCAAA TgCCTTTAAC
                 Consensus  ********** *******-** ********** ********** *-********

                            501                                                550
     msa221059.2{245_H36B}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAtAATAAT GGTGATTTAA
 msa221059.2{245_JM9130013} AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAtAATAAT GGTGATTTAA
   msa221059.2{245_1169NT}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAtAATAAT GGTGATTTAA
      msa221059.2{245_090}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TaAtAATAAT GGTGATTTAA
   msa221059.2{245_CJB110}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TaAtAATAAT GGTGATTTAA
   msa221059.2{245_18RS21}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
     msa221059.2{245_2603}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
     msa221059.2{245_A909}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
     msa221059.2{245_COH1}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
     msa221059.2{245_M732}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
     msa221059.2{245_M781}  AGATAAAAAA AGTTTCGCTA GTCTTATTAT TgAcAATAAT GGTGATTTAA
                 Consensus  ********** ********** ********** *-*-****** **********

                            551                                     591
     msa221059.2{245_H36B}  TAACTTTAAA AGAGCAAATg TTGGATGCTC TTCAACGTTT A
 msa221059.2{245_JM9130013} TAACTTTAAA AGAGCAAATg TTGGATGCTC TTCAACGTTT A
   msa221059.2{245_1169NT}  TAACTTTAAA AGAGCAAATg TTGGATGCTC TTCAACGTTT A
      msa221059.2{245_090}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
   msa221059.2{245_CJB110}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
   msa221059.2{245_18RS21}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
     msa221059.2{245_2603}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
     msa221059.2{245_A909}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
     msa221059.2{245_COH1}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
```

Table 57: Comparative Sequences relating to SAG 1488

```
msa221059.2{245_M732}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
msa221059.2{245_M781}  TAACTTTAAA AGAGCAAATa TTGGATGCTC TTCAACGTTT A
            Consensus  ********** *********- ********** ********** *
```

SEQ ID NO: 5712
STRAIN 2603 frame: 1
MLMTKIIGLTGGIASGKSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI
LDADGELDRPKLSQMIFANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLI
EEKYIKWFDEIWLVFVDKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNN
GDLITLKEQILDALQRL

SEQ ID NO: 5713
STRAIN 090 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFVDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIINNNGDLITLKEQILDALQR
L

SEQ ID NO: 5714
STRAIN A909 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNNGDLITLKEQILDALQR
L

SEQ ID NO: 5715
STRAIN H36B frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKSFASLIIDNNGDLITLKEQMLDALQR
L

SEQ ID NO: 5716
STRAIN 18RS21 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNNGDLITLKEQILDALQR
L

SEQ ID NO: 5717
STRAIN M732 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNNGDLITLKEQILDALQR
L

SEQ ID NO: 5718
STRAIN COH1 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNNGDLITLKEQILDALQR
L

SEQ ID NO: 5719
STRAIN M781 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIIDNNGDLITLKEQILDALQR
L

SEQ ID NO: 5720
STRAIN CJB110 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFVDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKSFASLIINNNGDLITLKEQILDALQR
L

SEQ ID NO: 5721
STRAIN 1169NT frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKSFASLIIDNNGDLITLKEQMLDALQR
L

SEQ ID NO: 5722
STRAIN JM9130013 frame: 1
KSTVTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEILDADGELDRPKLSQMI
FANPDNMKTSARLQNSIIRQELACQRDQLKQTEEIFFMDIPLLIEEKYIKWFDEIWLVFV
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKSFASLIIDNNGDLITLKEQMLDALQR
L

Table 57: Comparative Sequences relating to SAG 1488

```
PRETTY of: /biotmp/msa221398.2{*}   February 10, 2003 07:15  ..

                            1                                                   50
      msa221398.2{245_090}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
   msa221398.2{245_CJB110}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
   msa221398.2{245_1169NT}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_H36B}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_JM9130013}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
   msa221398.2{245_18RS21}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_2603}  mlmtkiiglt ggiasgKSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_A909}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_COH1}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_M732}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
     msa221398.2{245_M781}  ---------- ------KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
                 Consensus  ********** ********** ********** ********** **********

                            51                                                 100
      msa221398.2{245_090}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
   msa221398.2{245_CJB110}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
   msa221398.2{245_1169NT}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_H36B}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_JM9130013}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
   msa221398.2{245_18RS21}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_2603}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_A909}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_COH1}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_M732}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
     msa221398.2{245_M781}  ALLEWLGPEI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
                 Consensus  ********** ********** ********** ********** **********

                            101                                                150
      msa221398.2{245_090}  QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
   msa221398.2{245_CJB110}  QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
   msa221398.2{245_1169NT}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_H36B}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_JM9130013}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
   msa221398.2{245_18RS21}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_2603}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_A909}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_COH1}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_M732}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
     msa221398.2{245_M781}  QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
                 Consensus  ********** ***_****** ********** ********** **********

                            151                                             197
      msa221398.2{245_090}  YSREEAELRL SHQmPLTDKK SFASLIInNN GDLITLKEQi LDALQRL
   msa221398.2{245_CJB110}  YSREEAELRL SHQmPLTDKK SFASLIInNN GDLITLKEQi LDALQRL
   msa221398.2{245_1169NT}  YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
     msa221398.2{245_H36B}  YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_JM9130013}  YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
   msa221398.2{245_18RS21}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
     msa221398.2{245_2603}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
     msa221398.2{245_A909}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
     msa221398.2{245_COH1}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
     msa221398.2{245_M732}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
     msa221398.2{245_M781}  YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
                 Consensus  ********** ***_****** *******_** *********_ *******
```

Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801
STRAIN 2603
ATGTTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCTTTTTATTG
GTAAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGTCTAAACGTGAAACGGTAGTC
CTTGTCATCATTTTCGGCTTGTTTGTTATTATATCTAATATAACAGGAATTGAAATAAAA
GGGGATCGAAGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTT
GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA
TCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCT
TTCTATATTGTCAGTTCAGTTCTAGTCGGCATTGTTAGCGGAAAGATTGGTGATAAGCTT
AAGGAAAACCATCTCTACCCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAA
AGTATCCAGATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTC
ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATTTTGAAAACT
TATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTTGAATTGACT
CGACAGACTCTGCCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGC
GAAATTATAAAGAGGCATACTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTA
TTAGCTCATATTGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGAC
TTATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAAGCGGCGATT
TCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGTAGTTCCTCTAAAAATAAAT
GATAAAACTGTGGGTGCCTTAAAAATGTACTTTGCAGGAGATAAGACAATGTCTGAGGTG
GAGGAAAACCTAGTCCTTGGTTTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATA
ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
AACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGTATTGATTCT
GATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTTAGAACAAGTTTGCAGGGT
GGTCAGGATCGTGAGGTAACGCTTGAGCAAGAAAAATCACATGTGGATGCTTATATGAAT
GTTGAAAAATTACGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAA
AAAATGAAGTTACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCT
TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTAT
TATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATACTATCATTGATAAATTA
GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC
AGGCTGAATTTATTATATGGTAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGT
ACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT
TCT

SEQ ID NO. 5802
STRAIN 090
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCATCATTTTCGGCTTG
TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAG
TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCT
TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
GCTATTTGTTGGTATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCA
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
TTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
TGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACT
AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
TGGTGTTGGCCATGATCACCATATTGCAGGACAACCAGTCAAAACAGACC
TATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAA
GCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGT
AGTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTACT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGT
TTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
ACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGT
ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
TAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTT
ACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTAGACATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
GGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
AGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT
CT

SEQ ID NO. 5803
STRAIN A909
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTG
TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAG
TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
GCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCA
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
TTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT
TGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACT
AACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
TGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACT
TATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAA
GCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGT
AGTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTACT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGT
TTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
ACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGT
ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
TAGAACAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTT
ACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
GGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
AGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT
CT

SEQ ID NO. 5804
STRAIN H36B
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATG
ATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTGA
AGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTGT
TTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAGT
TTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
TGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAA
GGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCAT
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG
CTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCAT
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATTT
TGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT
GACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACTA
ACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATATT
GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT
ATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAAG
CGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGTA
GTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTACTT
TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGTT
TAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACAA
AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCAA
CCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGTA
TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
AGAACAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA
CCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTTT
CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
GTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
ACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC
AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
GTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGG
TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC
T

SEQ ID NO. 5805
STRAIN 18RS21
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATG
ATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTAGACAGTTAATTGA
AGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTGT
TTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAGT
TTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
TGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAA
GGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCAT
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG
CTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCAT
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATTT
TGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACTA
ACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATATT
GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT
ATCTAAAAGTGTTATTTTTGATGGCGAACCAAGaATTGCGCAAGATAAAG
CGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGTA
GTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTACTT
TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGTT
TAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACAA
AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCAA
CCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGTA
TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
AGAACAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA
CCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTTT
CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
GTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
ACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC
AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
GTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGG
TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC
T

SEQ ID NO. 5806
STRAIN M732
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATGAT
TTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTGAAG
AGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTTGTTT
GTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAGTTT
GGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTCTGACTCACTTGCTA
ATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTG
GTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGG
AAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCATTG
TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTTCA
ACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATGCT
ATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCATTC
CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATTTTG
AAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA
TGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA
CACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACTAAC
TTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATATTGG
TATTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTTAT
CTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAAGCG
GCGAtTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGTAGT
TCCTCTAAAAATAAATGATAAAACTGTGTGTGCCTTAAAAATGTACTTTG
CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGTTTA
GCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACAAAA
TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCAACC
CTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGTATT
GATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTTAG
AACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGAAA
AATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTGAT
AAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTACC
GCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTTTCA
AAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGT
CATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC
TATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGGACAG
GTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT
GTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGGTA
TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTCT

SEQ ID NO. 5807
STRAIN COH1
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTAT
TATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAA
TTGAAGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGC
TTGTTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCG
AAGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTCTGACTCAC
TTGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGA
CCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTT
TCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCG
GCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTAC
CCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCA
GATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTG
TCATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCG
ATTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC
GAGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAG
GTTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCAT
ACTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCA
TATTGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAG
ACTTATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGAT
AAAGCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTAT
TGTAGTTCCTCTAAAAATAAATGATAAAACTGTGTGTGCCTTAAAAATGT

Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTT
GGTTTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGA
ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA
TCAACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATC
CGTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTT
TTTTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGC
AAGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTC
CCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAA
GTTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATG
CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCA
GATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTC
AGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGG
GGACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATAT
GGTAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGT
TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTA
ATTCT

SEQ ID NO. 5808
STRAIN M781
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTA
TGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATT
GAAGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCTT
GTTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAA
GTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTCTGACTCACTT
GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACC
TCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTC
AAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGC
ATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCC
TTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGA
TGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTC
ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGAT
TTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGtTCAAACGA
GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGT
TTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATAC
TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATA
TTGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGAC
TTATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAA
AGCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTG
TAGTTCCTCTAAAAATAAATGATAAAACTGTGTGTGCCTTAAAAATGTAC
TTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGG
TTTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAAC
AAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
AACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCG
TATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT
TTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAA
GAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCC
TGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGT
TACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCT
TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA
TGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG
ATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGG
ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGG
TAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTT
GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT
TCT

SEQ ID NO. 5809
STRAIN CJB110
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCATCATTTTCGGCTTG
TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGAAG
TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCCATTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCT
TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
GCTATTTGTTGGTATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCA
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
TTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
TGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACT
AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
TGGTGTTGGCCATGATCACCATATTGCAGGACAACCAGTCAAAACAGACC
TATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATAAA
GCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGT
AGTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTACT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTGGT
TTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
ACCCTCATTTTTTCTTTAATGCCATTAACACAATTAGTGCATTAATCCGT
ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTT
ACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTAGACATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
GGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
AGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT
CT

SEQ ID NO. 5810
STRAIN 1169NT
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATT
ATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAAT
TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCATCATTTTCGGCT
TGTTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGA
AGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACT
TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTT
CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGG
CATTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAG
ATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGT
CATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGA
TTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
TTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATA
CTAATTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCAT
ATTGGTGTTGGCCATGATCACCATATTGCAGGACAACCAGTCAAAACAGA
CCTATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATA
AAGCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATT
GTAGTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTA
CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTG
GTTTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAA
CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
CAACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCC
GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
TTTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCA
AGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
CTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAG
TTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGC
TTTTAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG
ATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA
GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG
TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
GTAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT
TGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAA
TTCT

SEQ ID NO. 5810
STRAIN JM9130013
TTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATT
ATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAAT
TGAAGAGCGGTCTAAACGTGAAACGGTAGTCCTTGTCATCATTTTCGGCT
TGTTTGTTATTATATCTAATATAACAGGAATTGAAATAAAAGGGGATCGA
AGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACT
TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTT
CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTAGTCGG
CATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAG
ATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGT
CATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGA
TTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
TTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATA
CTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCAT
ATTGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGA
CTTATCTAAAAGTGTTATTTTTGATGGCGAACCAAGAATTGCGCAAGATA
AAGCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATT
GTAGTTCCTCTAAAAATAAATGATAAAACTGTGGGTGCCTTAAAAATGTA
CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTTG
GTTTAGCGCAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGAA
CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
CAACCCTCATTTCTTCTTTAATGCCATTAACACAATTAGTGCATTAATCC
GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
TTTAGAACAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCA
agAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
CTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAG
TTACCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGC
TTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

```
ATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA
GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG
TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
GTAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT
TGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAA
TTCT
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MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa442667.2{*}   January 13, 2003 06:34  ..

                                    1                                                   50
     msa442667.2{248_18RS21}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_2603}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_A909}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_H36B}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
  msa442667.2{248_JM9130013}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_COH1}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_M781}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
       msa442667.2{248_M732}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
        msa442667.2{248_090}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
     msa442667.2{248_CJB110}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
     msa442667.2{248_1169NT}        TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
                   Consensus        ********** ********** ********** ********** **********

                                    51                                                 100
     msa442667.2{248_18RS21}        TTTATTGGTA AATAATAGTT ATTTtAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_2603}        TTTATTGGTA AATAATAGTT ATTTtAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_A909}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_H36B}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
  msa442667.2{248_JM9130013}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_COH1}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_M781}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
       msa442667.2{248_M732}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
        msa442667.2{248_090}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
     msa442667.2{248_CJB110}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
     msa442667.2{248_1169NT}        TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
                   Consensus        ********** ********** ****_***** ********** **********

                                    101                                                150
     msa442667.2{248_18RS21}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_2603}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_A909}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_H36B}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
  msa442667.2{248_JM9130013}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_COH1}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_M781}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
       msa442667.2{248_M732}        AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
        msa442667.2{248_090}        AACGTGAAAC GGTAGTaCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
     msa442667.2{248_CJB110}        AACGTGAAAC GGTAGTaCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
     msa442667.2{248_1169NT}        AACGTGAAAC GGTAGTaCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
                   Consensus        ********** ******_*** ********** ********** **********

                                    151                                                200
     msa442667.2{248_18RS21}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_2603}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_A909}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_H36B}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
  msa442667.2{248_JM9130013}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_COH1}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_M781}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
       msa442667.2{248_M732}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
        msa442667.2{248_090}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
     msa442667.2{248_CJB110}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
     msa442667.2{248_1169NT}        TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
                   Consensus        ********** ********** ********** ********** **********

                                    201                                                250
     msa442667.2{248_18RS21}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_2603}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_A909}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_H36B}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
  msa442667.2{248_JM9130013}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_COH1}        CCCTTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_M781}        CCCTTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
       msa442667.2{248_M732}        CCCTTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
        msa442667.2{248_090}        CCCTTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
     msa442667.2{248_CJB110}        CCCTTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
     msa442667.2{248_1169NT}        CCCTTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
                   Consensus        ********** ********** *_******** ********** **********

                                    251                                                300
     msa442667.2{248_18RS21}        CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
       msa442667.2{248_2603}        CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
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Table 58: Comparative Sequences relating to SAG0182

```
     msa442667.2{248_A909}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
     msa442667.2{248_H36B}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
msa442667.2{248_JM9130013}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
     msa442667.2{248_COH1}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
     msa442667.2{248_M781}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
     msa442667.2{248_M732}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
      msa442667.2{248_090}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
   msa442667.2{248_CJB110}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
   msa442667.2{248_1169NT}   CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTTGGATCA
                 Consensus   ********** ********** ********** ********** **********

                             301                                                350
   msa442667.2{248_18RS21}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_2603}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_A909}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_H36B}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
msa442667.2{248_JM9130013}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_COH1}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_M781}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
     msa442667.2{248_M732}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
      msa442667.2{248_090}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
   msa442667.2{248_CJB110}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
   msa442667.2{248_1169NT}   ATTGTTGGTT TTATTGGAGG AGTTCATCGC TTTTTTCAAG GAAGCTTTTC
                 Consensus   ********** ********** ********** ********** **********

                             351                                                400
   msa442667.2{248_18RS21}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_2603}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_A909}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_H36B}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
msa442667.2{248_JM9130013}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_COH1}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_M781}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
     msa442667.2{248_M732}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
      msa442667.2{248_090}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
   msa442667.2{248_CJB110}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTtAGCGGAA
   msa442667.2{248_1169NT}   AGGTTCTTTC TATATTGTCA GTTCAGTTCT AGTCGGCATT GTgAGCGGAA
                 Consensus   ********** ********** ********** ********** **_*******

                             401                                                450
   msa442667.2{248_18RS21}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_2603}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_A909}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_H36B}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
msa442667.2{248_JM9130013}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_COH1}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_M781}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
     msa442667.2{248_M732}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
      msa442667.2{248_090}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
   msa442667.2{248_CJB110}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
   msa442667.2{248_1169NT}   AGATTGGTGA TAAGCTTAAG GAAAACCATC TCTACCCTTC AACAAGCCAA
                 Consensus   ********** ********** ********** ********** **********

                             451                                                500
   msa442667.2{248_18RS21}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_2603}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_A909}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_H36B}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
msa442667.2{248_JM9130013}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_COH1}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_M781}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
     msa442667.2{248_M732}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
      msa442667.2{248_090}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
   msa442667.2{248_CJB110}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
   msa442667.2{248_1169NT}   GTTATTTTAA TTAGTATTAT TGCCGAAAGT ATCCAGATGC TATTTGTTGG
                 Consensus   ********** ********** ********** ********** **********

                             501                                                550
   msa442667.2{248_18RS21}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_2603}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_A909}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_H36B}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
msa442667.2{248_JM9130013}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_COH1}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_M781}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
     msa442667.2{248_M732}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
      msa442667.2{248_090}   tATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
   msa442667.2{248_CJB110}   tATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
   msa442667.2{248_1169NT}   cATTTTTACA GGATGGGAAC TTGTCAAAAT GATTGTCATT CCAATGATGA
                 Consensus   -********* ********** ********** ********** **********

                             551                                                600
   msa442667.2{248_18RS21}   TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
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Table 58: Comparative Sequences relating to SAG0182

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     msa442667.2{248_2603}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
     msa442667.2{248_A909}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
     msa442667.2{248_H36B}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
msa442667.2{248_JM9130013}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
     msa442667.2{248_COH1}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
     msa442667.2{248_M781}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
     msa442667.2{248_M732}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
      msa442667.2{248_090}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
   msa442667.2{248_CJB110}  TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
  msa442667.2{248_1169NT}   TTTTAAATAG TTTAGGTTCC ACACTTTTCC TTGCGATTTT GAAAACTTAT
                 Consensus  ********** ********** ********** ********** **********

                            601                                               650
   msa442667.2{248_18RS21}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_2603}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_A909}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_H36B}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
msa442667.2{248_JM9130013}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_COH1}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_M781}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
     msa442667.2{248_M732}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
      msa442667.2{248_090}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
   msa442667.2{248_CJB110}  TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
  msa442667.2{248_1169NT}   TTGTCAAATG AAAGTCAGTT ACGCGCAGTT CAAACGAGAG ATGTTCTTGA
                 Consensus  ********** ********** ********** ********** **********

                            651                                               700
   msa442667.2{248_18RS21}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_2603}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_A909}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_H36B}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
msa442667.2{248_JM9130013}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_COH1}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_M781}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
     msa442667.2{248_M732}  ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
      msa442667.2{248_090}  ATTGACTCGA CAGACTCTGC CCTACCTcAG ACAAGGTTTG ACACCGCAAT
   msa442667.2{248_CJB110}  ATTGACTCGA CAGACTCTGC CCTACCTcAG ACAAGGTTTG ACACCGCAAT
  msa442667.2{248_1169NT}   ATTGACTCGA CAGACTCTGC CCTACCTtAG ACAAGGTTTG ACACCGCAAT
                 Consensus  ********** ********** *******-** ********** **********

                            701                                               750
   msa442667.2{248_18RS21}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_2603}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_A909}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_H36B}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
msa442667.2{248_JM9130013}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_COH1}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_M781}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
     msa442667.2{248_M732}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
      msa442667.2{248_090}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
   msa442667.2{248_CJB110}  CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA cTTTGATGCT
  msa442667.2{248_1169NT}   CTGCTAGGAG CGTTTGCGAA ATTATAAAGA GGCATACTAA tTTTGATGCT
                 Consensus  ********** ********** ********** ********** -*********

                            751                                               800
   msa442667.2{248_18RS21}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_2603}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_A909}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_H36B}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
msa442667.2{248_JM9130013}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_COH1}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_M781}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
     msa442667.2{248_M732}  GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTaTTGGCCA
      msa442667.2{248_090}  GTaGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
   msa442667.2{248_CJB110}  GTaGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
  msa442667.2{248_1169NT}   GTgGGATTAA CAGATCGGTC AAACGTATTA GCTCATATTG GTgTTGGCCA
                 Consensus  **-******* ********** ********** ********** **-*******

                            801                                               850
   msa442667.2{248_18RS21}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_2603}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_A909}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_H36B}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
msa442667.2{248_JM9130013}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_COH1}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_M781}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
     msa442667.2{248_M732}  TGATCACCAT ATTGCAGGAC AACCgGTCAA AACAGACtTA TCTAAAAGTG
      msa442667.2{248_090}  TGATCACCAT ATTGCAGGAC AACCaGTCAA AACAGACcTA TCTAAAAGTG
   msa442667.2{248_CJB110}  TGATCACCAT ATTGCAGGAC AACCaGTCAA AACAGACcTA TCTAAAAGTG
  msa442667.2{248_1169NT}   TGATCACCAT ATTGCAGGAC AACCaGTCAA AACAGACcTA TCTAAAAGTG
                 Consensus  ********** ********** ****-***** *******-** **********

                            851                                               900
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Table 58: Comparative Sequences relating to SAG0182

```
    msa442667.2{248_18RS21}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_2603}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_A909}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_H36B}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
 msa442667.2{248_JM9130013}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_COH1}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_M781}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
      msa442667.2{248_M732}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
       msa442667.2{248_090}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
    msa442667.2{248_CJB110}  TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
   msa442667.2{248_1169NT}   TTATTTTTGA TGGCGAACCA AGAATTGCGC AAGATAAAGC GGCGATTTCT
                  Consensus  ********** ********** ********** ********** **********

                             901                                                950
    msa442667.2{248_18RS21}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_2603}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_A909}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_H36B}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
 msa442667.2{248_JM9130013}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_COH1}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_M781}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
      msa442667.2{248_M732}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
       msa442667.2{248_090}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
    msa442667.2{248_CJB110}  TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
   msa442667.2{248_1169NT}   TGTCCAGATC ACAACTGTCA GTTAAATTCT GCTATTGTAG TTCCTCTAAA
                  Consensus  ********** ********** ********** ********** **********

                             951                                               1000
    msa442667.2{248_18RS21}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_2603}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_A909}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_H36B}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
 msa442667.2{248_JM9130013}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_COH1}  AATAAATGAT AAAACTGTGt GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_M781}  AATAAATGAT AAAACTGTGt GTGCCTTAAA AATGTACTTT GCAGGAGATA
      msa442667.2{248_M732}  AATAAATGAT AAAACTGTGt GTGCCTTAAA AATGTACTTT GCAGGAGATA
       msa442667.2{248_090}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
    msa442667.2{248_CJB110}  AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
   msa442667.2{248_1169NT}   AATAAATGAT AAAACTGTGg GTGCCTTAAA AATGTACTTT GCAGGAGATA
                  Consensus  ********** *********- ********** ********** **********

                             1001                                              1050
    msa442667.2{248_18RS21}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_2603}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_A909}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_H36B}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
 msa442667.2{248_JM9130013}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_COH1}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_M781}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
      msa442667.2{248_M732}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
       msa442667.2{248_090}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
    msa442667.2{248_CJB110}  AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
   msa442667.2{248_1169NT}   AGACAATGTC TGAGGTGGAG GAAAACCTAG TCCTTGGTTT AGCGCAAATA
                  Consensus  ********** ********** ********** ********** **********

                             1051                                              1100
    msa442667.2{248_18RS21}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_2603}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_A909}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_H36B}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
 msa442667.2{248_JM9130013}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_COH1}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_M781}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
      msa442667.2{248_M732}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
       msa442667.2{248_090}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
    msa442667.2{248_CJB110}  TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
   msa442667.2{248_1169NT}   TTTTCAGGAC AACTGGCAAT GGGGATAACA GAGGAACAAA ATAAGTTAGC
                  Consensus  ********** ********** ********** ********** **********

                             1101                                              1150
    msa442667.2{248_18RS21}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_2603}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_A909}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_H36B}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
 msa442667.2{248_JM9130013}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_COH1}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_M781}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
      msa442667.2{248_M732}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
       msa442667.2{248_090}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
    msa442667.2{248_CJB110}  CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTtT
   msa442667.2{248_1169NT}   CAGTATGGCA GAGATAAAGG CTTTACAAGC ACAAATCAAC CCTCATTTcT
                  Consensus  ********** ********** ********** ********** ********-*
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Table 58: Comparative Sequences relating to SAG0182

```
                                 1151                                                   1200
       msa442667.2{248_18RS21}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_2603}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_A909}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_H36B}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
     msa442667.2{248_JM9130013}  TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_COH1}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_M781}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
         msa442667.2{248_M732}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
          msa442667.2{248_090}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
       msa442667.2{248_CJB110}   TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
      msa442667.2{248_1169NT}    TCTTTAATGC CATTAACACA ATTAGTGCAT TAATCCGTAT TGATTCTGAT
                    Consensus    ********** ********** ********** ********** **********

                                 1201                                                   1250
       msa442667.2{248_18RS21}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_2603}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_A909}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_H36B}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
     msa442667.2{248_JM9130013}  AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_COH1}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_M781}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
         msa442667.2{248_M732}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
          msa442667.2{248_090}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
       msa442667.2{248_CJB110}   AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
      msa442667.2{248_1169NT}    AAAGCACGTT ATGCACTGAT GCAGTTAAGT ACTTTTTTTA GAACAAGTTT
                    Consensus    ********** ********** ********** ********** **********

                                 1251                                                   1300
       msa442667.2{248_18RS21}   GCAgGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_2603}   GCAgGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_A909}   GCAgGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_H36B}   GCAgGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
     msa442667.2{248_JM9130013}  GCAgGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_COH1}   GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_M781}   GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
         msa442667.2{248_M732}   GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
          msa442667.2{248_090}   GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
       msa442667.2{248_CJB110}   GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
      msa442667.2{248_1169NT}    GCAaGGTGGT CAGGATCGTG AGGTAACGCT TGAGCAAGAA AAATCACATG
                    Consensus    ***-****** ********** ********** ********** **********

                                 1301                                                   1350
       msa442667.2{248_18RS21}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_2603}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_A909}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_H36B}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
     msa442667.2{248_JM9130013}  TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_COH1}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_M781}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
         msa442667.2{248_M732}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
          msa442667.2{248_090}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
       msa442667.2{248_CJB110}   TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
      msa442667.2{248_1169NT}    TGGATGCTTA TATGAATGTT GAAAAATTAC GTTTCCCTGA TAAATATCAG
                    Consensus    ********** ********** ********** ********** **********

                                 1351                                                   1400
       msa442667.2{248_18RS21}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CaCCTTTTGG
         msa442667.2{248_2603}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CaCCTTTTGG
         msa442667.2{248_A909}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CaCCTTTTGG
         msa442667.2{248_H36B}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CaCCTTTTGG
     msa442667.2{248_JM9130013}  TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CaCCTTTTGG
         msa442667.2{248_COH1}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
         msa442667.2{248_M781}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
         msa442667.2{248_M732}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
          msa442667.2{248_090}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
       msa442667.2{248_CJB110}   TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
      msa442667.2{248_1169NT}    TTATCTTATG ATATTAGTGC ACCAGAAAAA ATGAAGTTAC CgCCTTTTGG
                    Consensus    ********** ********** ********** ********** *-********

                                 1401                                                   1450
       msa442667.2{248_18RS21}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_2603}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_A909}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_H36B}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
     msa442667.2{248_JM9130013}  TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_COH1}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_M781}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
         msa442667.2{248_M732}   TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTc AAAGAACGTA
          msa442667.2{248_090}   TTTACAGGTA CTGGTAGAGA ATGCAGTTaG ACATGCTTTc AAAGAACGTA
       msa442667.2{248_CJB110}   TTTACAGGTA CTGGTAGAGA ATGCAGTTaG ACATGCTTTc AAAGAACGTA
      msa442667.2{248_1169NT}    TTTACAGGTA CTGGTAGAGA ATGCAGTTcG ACATGCTTTt AAAGAACGTA
                    Consensus    ********** ********** ********-* *********- **********
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Table 58: Comparative Sequences relating to SAG0182

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                              1451                                                1500
     msa442667.2{248_18RS21}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_2603}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_A909}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_H36B}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
   msa442667.2{248_JM9130013}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_COH1}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_M781}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
       msa442667.2{248_M732}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
        msa442667.2{248_090}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
     msa442667.2{248_CJB110}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
    msa442667.2{248_1169NT}  AGACGGACAA CCATATATTG GTTCAAATAA AGCCAGATGG TCATTATTAT
                   Consensus  ********** ********** ********** ********** **********

                              1501                                                1550
     msa442667.2{248_18RS21}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_2603}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_A909}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_H36B}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
   msa442667.2{248_JM9130013}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_COH1}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_M781}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
       msa442667.2{248_M732}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
        msa442667.2{248_090}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
     msa442667.2{248_CJB110}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
    msa442667.2{248_1169NT}  TGTGTTTCTG TTAGTGACAA TGGACAAGGA ATCTCAGATA CTATCATTGA
                   Consensus  ********** ********** ********** ********** **********

                              1551                                                1600
     msa442667.2{248_18RS21}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
       msa442667.2{248_2603}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
       msa442667.2{248_A909}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
       msa442667.2{248_H36B}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
   msa442667.2{248_JM9130013}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
       msa442667.2{248_COH1}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGgACA GGTACTGCTC
       msa442667.2{248_M781}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGgACA GGTACTGCTC
       msa442667.2{248_M732}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGgACA GGTACTGCTC
        msa442667.2{248_090}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
     msa442667.2{248_CJB110}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
    msa442667.2{248_1169NT}  TAAATTAGGT CAAGAAACAG TTGCAGAGAG TAAGGGtACA GGTACTGCTC
                   Consensus  ********** ********** ********** ******_*** **********

                              1601                                                1650
     msa442667.2{248_18RS21}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_2603}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_A909}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_H36B}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
   msa442667.2{248_JM9130013}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_COH1}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_M781}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
       msa442667.2{248_M732}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
        msa442667.2{248_090}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
     msa442667.2{248_CJB110}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
    msa442667.2{248_1169NT}  TAGTTAATCT AAATAACAGG CTGAATTTAT TATATGGTAG TGTAAGTTGC
                   Consensus  ********** ********** ********** ********** **********

                              1651                                                1700
     msa442667.2{248_18RS21}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_2603}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_A909}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_H36B}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
   msa442667.2{248_JM9130013}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_COH1}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_M781}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
       msa442667.2{248_M732}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
        msa442667.2{248_090}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
     msa442667.2{248_CJB110}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
    msa442667.2{248_1169NT}  CTTCATTTTT CGAGCGACAA GAATGGTACA AAAGTTTGGT ATCGAATACC
                   Consensus  ********** ********** ********** ********** **********

                              1701                                    1740
     msa442667.2{248_18RS21}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_2603}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_A909}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_H36B}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
   msa442667.2{248_JM9130013}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_COH1}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_M781}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
       msa442667.2{248_M732}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
        msa442667.2{248_090}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
     msa442667.2{248_CJB110}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
    msa442667.2{248_1169NT}  TAATAGAATA AGGGAGGATG AGCATGAAAA TTTTAATTCT
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Table 58: Comparative Sequences relating to SAG0182

Consensus ********** ********** ********** **********

SEQ ID NO. 5811
STRAIN 2603 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5812
STRAIN 090 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5813
STRAIN A909 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5814
STRAIN H36B frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5815
STRAIN 18RS21 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5816
STRAIN M732 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGIGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818
STRAIN M781 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819
STRAIN CJB110 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820
STRAIN 1169NT frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821
STRAIN JM9130013 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNR
LNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEHENFNS

```
PRETTY of: /biotmp/msa442834.2{*}   January 13, 2003 06:47  ..

                              1                                                   50
      msa442834.2{248_090}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
   msa442834.2{248_1169NT}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
    msa442834.2{248_18RS21}   LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_2603}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_A909}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
   msa442834.2{248_CJB110}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_H36B}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
msa442834.2{248_JM9130013}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_COH1}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_M781}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
     msa442834.2{248_M732}    LMVLLFQRLG IIMILAFLLV NNSYFRQLIE ERSKRETVVL VIIFGLFVII
                 Consensus    ********** ********** ********** ********** **********

                              51                                                 100
      msa442834.2{248_090}    SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
   msa442834.2{248_1169NT}    SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
```

Table 58: Comparative Sequences relating to SAG0182

```
      msa442834.2{248_18RS21}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_2603}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_A909}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
      msa442834.2{248_CJB110}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_H36B}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
   msa442834.2{248_JM9130013}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_COH1}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_M781}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
        msa442834.2{248_M732}  SNITGIEIKG DRSLVERPFL TTISHSDSLA NTRTLVITTA SLVGGPLVGS
                    Consensus  ********** ********** ********** ********** **********

                               101                                              150
         msa442834.2{248_090}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
      msa442834.2{248_1169NT}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
      msa442834.2{248_18RS21}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_2603}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_A909}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
      msa442834.2{248_CJB110}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_H36B}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
   msa442834.2{248_JM9130013}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_COH1}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_M781}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
        msa442834.2{248_M732}  IVGFIGGVHR FFQGSFSGSF YIVSSVLVGI VSGKIGDKLK ENHLYPSTSQ
                    Consensus  ********** ********** ********** ********** **********

                               151                                              200
         msa442834.2{248_090}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
      msa442834.2{248_1169NT}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
      msa442834.2{248_18RS21}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_2603}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_A909}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
      msa442834.2{248_CJB110}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_H36B}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
   msa442834.2{248_JM9130013}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_COH1}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_M781}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
        msa442834.2{248_M732}  VILISIIAES IQMLFVGIFT GWELVKMIVI PMMILNSLGS TLFLAILKTY
                    Consensus  ********** ********** ********** ********** **********

                               201                                              250
         msa442834.2{248_090}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
      msa442834.2{248_1169NT}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
      msa442834.2{248_18RS21}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_2603}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_A909}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
      msa442834.2{248_CJB110}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_H36B}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
   msa442834.2{248_JM9130013}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_COH1}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_M781}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
        msa442834.2{248_M732}  LSNESQLRAV QTRDVLELTR QTLPYLRQGL TPQSARSVCE IIKRHTNFDA
                    Consensus  ********** ********** ********** ********** **********

                               251                                              300
         msa442834.2{248_090}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
      msa442834.2{248_1169NT}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
      msa442834.2{248_18RS21}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_2603}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_A909}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
      msa442834.2{248_CJB110}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_H36B}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
   msa442834.2{248_JM9130013}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_COH1}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_M781}  VGLTDRSNVL AHIGvGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
        msa442834.2{248_M732}  VGLTDRSNVL AHIGiGHDHH IAGQPVKTDL SKSVIFDGEP RIAQDKAAIS
                    Consensus  ********** ****-***** ********** ********** **********

                               301                                              350
         msa442834.2{248_090}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
      msa442834.2{248_1169NT}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
      msa442834.2{248_18RS21}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_2603}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_A909}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
      msa442834.2{248_CJB110}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_H36B}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
   msa442834.2{248_JM9130013}  CPDHNCQLNS AIVVPLKIND KTVgALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_COH1}  CPDHNCQLNS AIVVPLKIND KTVcALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_M781}  CPDHNCQLNS AIVVPLKIND KTVcALKMYF AGDKTMSEVE ENLVLGLAQI
        msa442834.2{248_M732}  CPDHNCQLNS AIVVPLKIND KTVcALKMYF AGDKTMSEVE ENLVLGLAQI
                    Consensus  ********** ********** ***-****** ********** **********

                               351                                              400
         msa442834.2{248_090}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
```

Table 58: Comparative Sequences relating to SAG0182

```
     msa442834.2{248_1169NT}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
     msa442834.2{248_18RS21}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_2603}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_A909}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
      msa442834.2{248_CJB110}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_H36B}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
   msa442834.2{248_JM9130013}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_COH1}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_M781}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
        msa442834.2{248_M732}  FSGQLAMGIT EEQNKLASMA EIKALQAQIN PHFFFNAINT ISALIRIDSD
                    Consensus  ********** ********** ********** ********** **********

                               401                                               450
         msa442834.2{248_090}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
      msa442834.2{248_1169NT}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
      msa442834.2{248_18RS21}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_2603}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_A909}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
      msa442834.2{248_CJB110}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_H36B}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
   msa442834.2{248_JM9130013}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_COH1}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_M781}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
        msa442834.2{248_M732}  KARYALMQLS TFFRTSLQGG QDREVTLEQE KSHVDAYMNV EKLRFPDKYQ
                    Consensus  ********** ********** ********** ********** **********

                               451                                               500
         msa442834.2{248_090}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
      msa442834.2{248_1169NT}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
      msa442834.2{248_18RS21}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_2603}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_A909}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
      msa442834.2{248_CJB110}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_H36B}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
   msa442834.2{248_JM9130013}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_COH1}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_M781}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
        msa442834.2{248_M732}  LSYDISAPEK MKLPPFGLQV LVENAVRHAF KERKTDNHIL VQIKPDGHYY
                    Consensus  ********** ********** ********** ********** **********

                               501                                               550
         msa442834.2{248_090}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
      msa442834.2{248_1169NT}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
      msa442834.2{248_18RS21}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_2603}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_A909}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
      msa442834.2{248_CJB110}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_H36B}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
   msa442834.2{248_JM9130013}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_COH1}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_M781}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
        msa442834.2{248_M732}  CVSVSDNGQG ISDTIIDKLG QETVAESKGT GTALVNLNNR LNLLYGSVSC
                    Consensus  ********** ********** ********** ********** **********

                               551                         580
         msa442834.2{248_090}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
      msa442834.2{248_1169NT}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
      msa442834.2{248_18RS21}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_2603}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_A909}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
      msa442834.2{248_CJB110}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_H36B}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
   msa442834.2{248_JM9130013}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_COH1}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_M781}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
        msa442834.2{248_M732}  LHFSSDKNGT KVWYRIPNRI REDEHENFNS
                    Consensus  ********** ********** **********
```

Table 59: Comparative Sequences relating to SAG2147

SEQ ID NO. 5901
STRAIN 2603
ATGAATAAAAGAAGAAAATTATCAAAATTGAATGTAAAAAAACATCATTTAGCTTATGGA
GCTATCACTTTAGTAGCCCTTTTTTCATGTATTTTGGCTGTAATGGTCATCTTTAAAAGT
TCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCA
AAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCT
TCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG
CAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAACACC
CCTGCTACCAGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCT
CAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAAATAcTGCAGGGGCTATTGGCTCA
GCAGCTGCAGCACAAATGGCTGCTGCAAcAGGAGTCCCTCAGTCTACTTGGGAAcATATT
ATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT
TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCT
ATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTACTAG

SEQ ID NO. 5902
STRAIN JM9130013
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAA
AGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGAATAAGGCAACAT
CTAAATCAAAAGTAGAAGGTGTAAAACAGGCTCCAAAACCAAGTTCTCAA
TCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGC
TGTAGAACAAGCAGTTGTAACAGAAAATACCCCTGCTACCAGTCAAGCAC
AACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAG
CCGAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGTTATTGGCTC
AGCAGCAGCAGCACAAATGGCTGCTGCAACGGGAGTTCCTCAGTCTACTT
GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAACGTTGCTAAT
GCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC
AGCTACAGTTCAGGATCAAGTTAATtCAGCTATTAAAGCTTATCGTGCTC
AAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5903
STRAIN 1169NT reverse complement
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCC
AAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCT
CCAAAACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCT
AATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACA
GAAAATACCCCTGCTACCAGTCAGGCACAACAAACTTATGCTGTTACTGAGACAACTTAC
AAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGCG
GTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG
GAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCT
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT
AATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5904
STRAIN 18RS21 reverse complement
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTC
GCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA
AACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTA
CAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAG
TTGTAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGCTGTTACTGAGA
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAAATACTG
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGT
CTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCT
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG
ATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5905
STRAIN 090 reverse complement
TAGCCAAAAAATCAAAAATGATTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAC
AGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAG
AAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTG
TAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAA
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAAATACTGCAG
GGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA
CTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAG
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

SEQ ID NO. 5906
STRAIN A909 reverse complement
AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCA
TCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTT
ACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAACACCCCTGCTACC
AGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAG
ACAAGTGGCCAAGTATTGAGTAATGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCA
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGT
GAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAATCAAGTTAATTCAGCTATTAAAGCT
TATCGTGCTCAAGGTTTATCA

SEQ ID NO. 5907
STRAIN CJB110 reverse complement
AATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG
AAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGA
GTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAACACCCCTGCTACCAGTCAGG
CACAACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAGACGAGTG
GCCAAGTATTGAGTAATGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA
TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA
ATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG
GTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTG
CTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5908
STRAIN COH1 reverse complement
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAA
AGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGA
TGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCA
ATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA
AGCAGTTGTAACAGAAAATACCCCTGCTACCAGTCAGGCACAACAAACTTATGCTGTTAC
TGAGACAACTTACAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAA
TACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC
TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA
TGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT
TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG
TTAC

SEQ ID NO. 5909
STRAIN H36B reverse complement
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGC
AGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGT
AGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAG
TTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGT
AGAACAAGCAGTTGTAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGC
TGTTACTGAGACAACTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA
TGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG
AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT
TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC
TACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTT

SEQ ID NO. 5910
STRAIN M732 reverse complement
AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGC
CAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGC
TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGC
TAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAC
AGAAAATACCCCTGCTACCAGTCAGGCACAACAAACTTATGCTGTTACTGAGACAACTTA
CAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGC
GGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG
GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC
TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGT
TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

SEQ ID NO. 5911
STRAIN M781 reverse complement
TCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA
TCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA
GCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGT
GAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGAAAATACCCCTGCTACCAGTCAGGCA
CAACAAACTTATGCTGTTACTGAGACAACTTACAAACCTGCTCAACACCAGACAAGTGGC
CAAGTATTGAGCAATGGAAATACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATG
GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT
GGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGT
TGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCT
CAAGGTTTATCAGCTTGGGGTTAC

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PRETTY of: /biotmp/msa519780.2{*}   March 10, 2003 06:25  ..

                           1                                                  50
     msa519780.2{25_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa519780.2{25_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa519780.2{25_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa519780.2{25_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa519780.2{25_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa519780.2{2603}  atgaataaaa gaagaaaatt atcaaaattg aatgtaaaaa aacatcattt
     msa519780.2{25_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa519780.2{25_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ********** ********** ********** **********

                           51                                                100
     msa519780.2{25_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

Table 59: Comparative Sequences relating to SAG2147

```
  msa519780.2{25_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa519780.2{25_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa519780.2{25_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa519780.2{25_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa519780.2{2603}  agcttatgga gctatcactt tagtagccct tttttcatgt attttggctg
    msa519780.2{25_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa519780.2{25_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus  ********** ********** ********** ********** **********

                          101                                                150
    msa519780.2{25_COH1}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
    msa519780.2{25_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~tc tttgtcaaaa
    msa519780.2{25_M732}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
  msa519780.2{25_1169NT}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
  msa519780.2{25_18RS21}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
    msa519780.2{25_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519780.2{25_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa519780.2{25_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~aatc tttgtcaaaa
       msa519780.2{2603}  taatggtcat ctttaaaagt tcacaagtta ctactgaatc tttgtcaaaa
    msa519780.2{25_H36B}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
msa519780.2{25_JM9130013}  ~~~~~~~~~~ ~~~~aaaagt tcacaagtta ctactgaatc tttgtcaaaa
               Consensus  ********** ****------ ---------- ---------- ----------

                          151                                                200
    msa519780.2{25_COH1}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
    msa519780.2{25_M781}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
    msa519780.2{25_M732}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
  msa519780.2{25_1169NT}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
  msa519780.2{25_18RS21}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
    msa519780.2{25_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~A AGGCgACATC
     msa519780.2{25_090}  ~~~~~~~~~~ ~~~~~~tagc caaaaaatca aaaatgattA AGGCgACATC
  msa519780.2{25_CJB110}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
       msa519780.2{2603}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
    msa519780.2{25_H36B}  gcagataaag ttcgcgtagc caaaaaatca aaaatgactA AGGCgACATC
msa519780.2{25_JM9130013}  gcagataaag ttcgcgtagc caaaaaatca aaaatgaatA AGGCaACATC
               Consensus  ---------- ---------- ---------- ---------* ****-*****

                          201                                                250
    msa519780.2{25_COH1}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
    msa519780.2{25_M781}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
    msa519780.2{25_M732}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
  msa519780.2{25_1169NT}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
  msa519780.2{25_18RS21}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
    msa519780.2{25_A909}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
     msa519780.2{25_090}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
  msa519780.2{25_CJB110}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
       msa519780.2{2603}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
    msa519780.2{25_H36B}  TAAATCAAAA GTAGAAGaTG TAAAACAGGC TCCAAAACct tctcaggcat
msa519780.2{25_JM9130013}  TAAATCAAAA GTAGAAGgTG TAAAACAGGC TCCAAAAC.. ..........
               Consensus  ********** *******-** ********** ********-- ----------

                          251                                                300
    msa519780.2{25_COH1}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
    msa519780.2{25_M781}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
    msa519780.2{25_M732}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
  msa519780.2{25_1169NT}  ctaatgaagt cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
  msa519780.2{25_18RS21}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
    msa519780.2{25_A909}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
     msa519780.2{25_090}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
  msa519780.2{25_CJB110}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
       msa519780.2{2603}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
    msa519780.2{25_H36B}  ctaatgaagc cccaaaatCA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
msa519780.2{25_JM9130013}  .......... ........CA AGTTCTCAAT CTACAGAAGC TAATTCTCAG
               Consensus  ---------- --------** ********** ********** **********

                          301                                                350
    msa519780.2{25_COH1}  CAACAAGTTA CTGCGAGTGA AGAGGCgGCT GTAGAACAAG CAGTTGTAAC
    msa519780.2{25_M781}  CAACAAGTTA CTGCGAGTGA AGAGGCgGCT GTAGAACAAG CAGTTGTAAC
    msa519780.2{25_M732}  CAACAAGTTA CTGCGAGTGA AGAGGCgGCT GTAGAACAAG CAGTTGTAAC
  msa519780.2{25_1169NT}  CAACAAGTTA CTGCGAGTGA AGAGGCgGCT GTAGAACAAG CAGTTGTAAC
  msa519780.2{25_18RS21}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
    msa519780.2{25_A909}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
     msa519780.2{25_090}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
  msa519780.2{25_CJB110}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
       msa519780.2{2603}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
    msa519780.2{25_H36B}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
msa519780.2{25_JM9130013}  CAACAAGTTA CTGCGAGTGA AGAGGCaGCT GTAGAACAAG CAGTTGTAAC
               Consensus  ********** ********** ******-*** ********** **********

                          351                                                400
    msa519780.2{25_COH1}  AGAAAAtACC CCTGCTACCA GTCAgGCACA ACAAaCTTAT GCTGTTACTG
    msa519780.2{25_M781}  AGAAAAtACC CCTGCTACCA GTCAgGCACA ACAAaCTTAT GCTGTTACTG
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Table 59: Comparative Sequences relating to SAG2147

```
     msa519780.2{25_M732}  AGAAAAtACC CCTGCTACCA GTCAgGCACA ACAAaCTTAT GCTGTTACTG
   msa519780.2{25_1169NT}  AGAAAAtACC CCTGCTACCA GTCAgGCACA ACAAaCTTAT GCTGTTACTG
   msa519780.2{25_18RS21}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
     msa519780.2{25_A909}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
      msa519780.2{25_090}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
   msa519780.2{25_CJB110}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
        msa519780.2{2603}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
     msa519780.2{25_H36B}  AGAAAAcACC CCTGCTACCA GTCAgGCACA ACAAgCTTAT GCTGTTACTG
msa519780.2{25_JM9130013}  AGAAAAtACC CCTGCTACCA GTCAaGCACA ACAAgCTTAT GCTGTTACTG
                Consensus  ******-*** ********** ****-***** ****-***** **********

                           401                                                450
     msa519780.2{25_COH1}  AGACAACTTA cAaACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGc
     msa519780.2{25_M781}  AGACAACTTA cAaACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGc
     msa519780.2{25_M732}  AGACAACTTA cAaACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGc
   msa519780.2{25_1169NT}  AGACAACTTA cAaACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGc
   msa519780.2{25_18RS21}  AGACAACTTA tAgACCTGCT CAACACCAGa CgAGTGGCCA AGTATTGAGt
     msa519780.2{25_A909}  AGACAACTTA tAgACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGt
      msa519780.2{25_090}  AGACAACTTA tAgACCTGCT CAACACCAGa CgAGTGGCCA AGTATTGAGt
   msa519780.2{25_CJB110}  AGACAACTTA tAgACCTGCT CAACACCAGa CgAGTGGCCA AGTATTGAGt
        msa519780.2{2603}  AGACAACTTA tAgACCTGCT CAACACCAGa CgAGTGGCCA AGTATTGAGt
     msa519780.2{25_H36B}  AGACAACTTA tAgACCTGCT CAACACCAGa CaAGTGGCCA AGTATTGAGt
msa519780.2{25_JM9130013}  AGACAACTTA tAgACCTGCT CAACACCAGc CgAGTGGCCA AGTATTGAGc
                Consensus  ********** -*-******* *********- *-******** *********-

                           451                                                500
     msa519780.2{25_COH1}  AATGGAAATA CTGCAGGGGc ggTcGGaTCt GCtGCtGCAG CACAAATGGC
     msa519780.2{25_M781}  AATGGAAATA CTGCAGGGGc ggTcGGaTCt GCtGCtGCAG CACAAATGGC
     msa519780.2{25_M732}  AATGGAAATA CTGCAGGGGc ggTcGGaTCt GCtGCtGCAG CACAAATGGC
   msa519780.2{25_1169NT}  AATGGAAATA CTGCAGGGGc ggTcGGaTCt GCtGCtGCAG CACAAATGGC
   msa519780.2{25_18RS21}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
     msa519780.2{25_A909}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
      msa519780.2{25_090}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
   msa519780.2{25_CJB110}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
        msa519780.2{2603}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
     msa519780.2{25_H36B}  AATGGAAATA CTGCAGGGGc taTtGGcTCa GCaGCtGCAG CACAAATGGC
msa519780.2{25_JM9130013}  AATGGAAATA CTGCAGGGGt taTtGGcTCa GCaGCaGCAG CACAAATGGC
                Consensus  ********** *********- --*-**-**- **-**-**** **********

                           501                                                550
     msa519780.2{25_COH1}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
     msa519780.2{25_M781}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
     msa519780.2{25_M732}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
   msa519780.2{25_1169NT}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
   msa519780.2{25_18RS21}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
     msa519780.2{25_A909}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
      msa519780.2{25_090}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
   msa519780.2{25_CJB110}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
        msa519780.2{2603}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
     msa519780.2{25_H36B}  TGCTGCAACa GGAGTcCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
msa519780.2{25_JM9130013}  TGCTGCAACg GGAGTtCCTC AGTCTACTTG GGAACATATT ATTGCCCGTG
                Consensus  *********- *****-**** ********** ********** **********

                           551                                                600
     msa519780.2{25_COH1}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
     msa519780.2{25_M781}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
     msa519780.2{25_M732}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
   msa519780.2{25_1169NT}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
   msa519780.2{25_18RS21}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
     msa519780.2{25_A909}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
      msa519780.2{25_090}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
   msa519780.2{25_CJB110}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
        msa519780.2{2603}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
     msa519780.2{25_H36B}  AATCAAATGG TAATCCTAAt GTTGCTAATG CCTCAGGAGC TTCAGGACTT
msa519780.2{25_JM9130013}  AATCAAATGG TAATCCTAAc GTTGCTAATG CCTCAGGAGC TTCAGGACTT
                Consensus  ********** *********- ********** ********** **********

                           601                                                650
     msa519780.2{25_COH1}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
     msa519780.2{25_M781}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
     msa519780.2{25_M732}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
   msa519780.2{25_1169NT}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
   msa519780.2{25_18RS21}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
     msa519780.2{25_A909}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGaAtcaagt
      msa519780.2{25_090}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgA~~~~~~
   msa519780.2{25_CJB110}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
        msa519780.2{2603}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
     msa519780.2{25_H36B}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
msa519780.2{25_JM9130013}  TTCCAAACGA TGCCAGGTTG GGGTTCAACA GCTACAGTTC AGgAtcaagt
                Consensus  ********** ********** ********** ********** **-*------

                           651                                                700
     msa519780.2{25_COH1}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
```

Table 59: Comparative Sequences relating to SAG2147

```
     msa519780.2{25_M781}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
     msa519780.2{25_M732}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
   msa519780.2{25_1169NT}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
   msa519780.2{25_18RS21}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
     msa519780.2{25_A909}  taattcagct attaaagctt atcgtgctca aggtttatca ~~~~~~~~~~
      msa519780.2{25_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa519780.2{25_CJB110}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
        msa519780.2{2603}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
     msa519780.2{25_H36B}  taattcagct attaaagctt ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa519780.2{25_JM9130013}  taattcagct attaaagctt atcgtgctca aggtttatca gcttggggtt
                Consensus  ---------- ---------- ---------- ---------- ----------

                           701
     msa519780.2{25_COH1}  ac~~~
     msa519780.2{25_M781}  ac~~~
     msa519780.2{25_M732}  a~~~~
   msa519780.2{25_1169NT}  ac~~~
   msa519780.2{25_18RS21}  ac~~~
     msa519780.2{25_A909}  ~~~~~
      msa519780.2{25_090}  ~~~~~
   msa519780.2{25_CJB110}  ac~~~
        msa519780.2{2603}  actag
     msa519780.2{25_H36B}  ~~~~~
msa519780.2{25_JM9130013}  ac~~~
                Consensus  --***
```

SEQ ID NO. 5912
STRAIN 2603 frame: 1
MNKRRKLSKLNVKKHHLAYGAITLVALFSCILAVMVIFKSSQVTTESLSKADKVRVAKKS
KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENT
PATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAIGSAAAAQMAAATGVPQSTWEHI
IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQGLSAWGY

SEQ ID NO. 5913
STRAIN 1169NT frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5914
STRAIN 18RS21 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5915
STRAIN 2603 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5916
STRAIN 090 frame: 3
AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVV
TENTPATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAIGSAAAAQMAAATGVPQST
WEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQ

SEQ ID NO. 5917
STRAIN A909 frame: 1
KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPAT
SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAIGSAAAAQMAAATGVPQSTWEHIIAR
ESNGNPNVANASGASGLFQTMPGWGSTATVQNQVNSAIKAYRAQGLS

SEQ ID NO. 5918
STRAIN CJB110 frame: 3
SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAIGSAAAAQM
AAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
QGLSAWGY

SEQ ID NO. 5919
STRAIN COH1 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5920
STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKA

SEQ ID NO. 5921
STRAIN M732 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWG

SEQ ID NO. 5922
STRAIN M781 frame: 4
SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAVGSAAAAQM
AAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
QGLSAWGY

SEQ ID NO. 5923
STRAIN JM9130013 frame: 1
KSSQVTTESLSKADKVRVAKKSKMNKATSKSKVEGVKQAPKPSSQSTEANSQQQVTASEE
AAVEQAVVTENTPATSQAQQAYAVTETTYRPAQHQPSGQVLSNGNTAGVIGSAAAAQMAA
ATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQG
LSAWGY

MSA Alignment Results: Pretty output

```
PRETTY of: /biotmp/msa519418.2{*}   March 10, 2003 06:15  ..

                                   1                                                      50
          msa519418.2{25_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa519418.2{25_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
          msa519418.2{25_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
          msa519418.2{25_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~SLSK
        msa519418.2{25_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
          msa519418.2{25_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
        msa519418.2{25_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
        msa519418.2{25_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~SLSK
          msa519418.2{25_2603}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
             msa519418.2{2603}  mnkrrklskl nvkkhhlayg aitlvalfsc ilavmvifKS SQVTTESLSK
          msa519418.2{25_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa519418.2{25_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~KS SQVTTESLSK
                     Consensus  ********** ********** ********** ********** **********

                                51                                                    100
          msa519418.2{25_090}   ~~~~~~akks kmiKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
          msa519418.2{25_H36B}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
          msa519418.2{25_COH1}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
          msa519418.2{25_M781}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
        msa519418.2{25_1169NT}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasnevpks SSQSTEANSQ
          msa519418.2{25_M732}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
        msa519418.2{25_18RS21}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
        msa519418.2{25_CJB110}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
          msa519418.2{25_2603}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
             msa519418.2{2603}  ADKVRVakks kmtKATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
          msa519418.2{25_A909}  ~~~~~~~~~~ ~~~KATSKSK VEdVKQAPKP sqasneapks SSQSTEANSQ
     msa519418.2{25_JM9130013}  ADKVRVakks kmnKATSKSK VEgVKQAPKP .......... SSQSTEANSQ
                     Consensus  ******---- ---******* **_******* ---------- **********

                                101                                                   150
          msa519418.2{25_090}   QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
          msa519418.2{25_H36B}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
          msa519418.2{25_COH1}  QQVTASEEAA VEQAVVTENT PATSQAQQtY AVTETTYkPA QHQtSGQVLS
          msa519418.2{25_M781}  QQVTASEEAA VEQAVVTENT PATSQAQQtY AVTETTYkPA QHQtSGQVLS
        msa519418.2{25_1169NT}  QQVTASEEAA VEQAVVTENT PATSQAQQtY AVTETTYkPA QHQtSGQVLS
          msa519418.2{25_M732}  QQVTASEEAA VEQAVVTENT PATSQAQQtY AVTETTYkPA QHQtSGQVLS
        msa519418.2{25_18RS21}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
        msa519418.2{25_CJB110}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
          msa519418.2{25_2603}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
             msa519418.2{2603}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
          msa519418.2{25_A909}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQtSGQVLS
     msa519418.2{25_JM9130013}  QQVTASEEAA VEQAVVTENT PATSQAQQaY AVTETTYrPA QHQpSGQVLS
                     Consensus  ********** ********** ********_* *******_** ***_******

                                151                                                   200
          msa519418.2{25_090}   NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
          msa519418.2{25_H36B}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
          msa519418.2{25_COH1}  NGNTAGavGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
          msa519418.2{25_M781}  NGNTAGavGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
        msa519418.2{25_1169NT}  NGNTAGavGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
          msa519418.2{25_M732}  NGNTAGavGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
        msa519418.2{25_18RS21}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
        msa519418.2{25_CJB110}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
```

Table 59: Comparative Sequences relating to SAG2147

```
    msa519418.2{25_2603}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
       msa519418.2{2603}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
    msa519418.2{25_A909}  NGNTAGaiGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
msa519418.2{25_JM9130013}  NGNTAGviGS AAAAQMAAAT GVPQSTWEHI IARESNGNPN VANASGASGL
               Consensus  ******--** ********** ********** ********** **********

                          201                                  234
     msa519418.2{25_090}  FQTMPGWGST ATVQ~~~~~~ ~~~~~~~~~~ ~~~~
    msa519418.2{25_H36B}  FQTMPGWGST ATVQDQVNSA IKA~~~~~~~ ~~~~
    msa519418.2{25_COH1}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
    msa519418.2{25_M781}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
  msa519418.2{25_1169NT}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
    msa519418.2{25_M732}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWG~
  msa519418.2{25_18RS21}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
  msa519418.2{25_CJB110}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
    msa519418.2{25_2603}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
       msa519418.2{2603}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
    msa519418.2{25_A909}  FQTMPGWGST ATVQnQVNSA IKAYRAQGLS ~~~~
msa519418.2{25_JM9130013}  FQTMPGWGST ATVQDQVNSA IKAYRAQGLS AWGY
               Consensus  ********** ********** ********** ****
```

Table 60: Comparative Sequences relating to SAG1945

SEQ ID NO. 6001
STRAIN 2603
ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTTCCATTATTTTT
ATAAGTGTTTTTACATACAGTATTAGCCAGCCTTCTAAACTACTTCCACCAAAAGAATTA
GTTATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAA
AAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGATTA
AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGAGGAAATTATACGCAATTT
GAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATGTTCATACTGTTATTCCA
GACTATATCCATCCAAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATT
GTAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCT
TCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTCACAA
CTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACTATGTT
AAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAA
TCAGTTGCAGAAGGAAAAATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTG
CAAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCA
TCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAAT
TTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGACCTATT
CGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAA
GAAGATTATCGCTATGTCACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATT
CGTAGAAATGCTGAT

SEQ ID NO. 6002
STRAIN 090
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGT
CCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAA
ATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG
ATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGA
GGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGT
ATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGTGATA
CGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAA
TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTC
CTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTT
TCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCA
AAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAA
ATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGA
TTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGT
GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATC
TTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTAT
TTATTAATTTTATGCTTtCTTTAgATGTTCAAAATGCCTTTGGGCAGTCA
ACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAA
AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTA
AGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAATGCT
GAT

SEQ ID NO. 6003
STRAIN A909
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAG
TTATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCT
TTTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGG
TCAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATA
TTTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTT
GAGTCTTACGTATCAAAGAATATTCATACTGTTATTCCAGATTATATCCA
TCCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTG
TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA
TTACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTC
CTCTAGTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTT
ACACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATT
AATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGA
AGGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGC
AAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
TTTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGA
AGCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCT
TTGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGT
AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
CTATGTCACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTC
GTAGAAATGCTGAT

SEQ ID NO. 6004
STRAIN H36B
TAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
CCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATACGGTATAAAA
GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAGTAA
GGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGAGGAAATTATACGC
AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT
CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
TACTATAAATGGGAGTGTCTTGATTGTAAATAAcGAATTAGTTAAGGGAC
TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTAAAAGGTAAA
ATTGCCTTTGCAGATCCGAATACTTCCTcTAGTGCTTTCTCACAACTCAC
TAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACT
ATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCT
TCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGTGGGGTTGAC
TTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCAATGTTTCTA
TTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAATTTTAT
GCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGAC
CTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT
ATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCATAAGGGCCA
AATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6005
STRAIN 18RS21
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAA
TAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATACG
GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCGgATATTTTCTTTGGAGGAAA
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA
AGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGTGATACGGCG
ACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGC
TAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTAA
AAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTCA
CAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGC
GTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCTT
CTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGTG
GGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCAA
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCGG
TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATT
AATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAG
TAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCAT
AAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6006
STRAIN M732
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATAT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTA
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCG
TAGAAATGCTGAT

SEQ ID NO. 6007
STRAIN COH1
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTT
ATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTT
TGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGC
AACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATT
TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
GTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATC
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATT
ACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCT
CTAGTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTAC
ACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAA
TGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAG
GAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAA
AAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTT
TGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG
CAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTT
GGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
ATGTCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGT
AGAAATGCTGAT

SEQ ID NO. 6008
STRAIN M781
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGA
GGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC
TAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTC
TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTC
TTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCGA
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
GCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTA
GTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACC
AATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGC
TATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAA
AAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAA
AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTTTGT
CCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAA
AGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGG
CAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAATGG
CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
TCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGTAGA
AATGCTGAT

SEQ ID NO. 6009
STRAIN CJB110
CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT
AAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGg
AAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
ATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTT
TGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT
ACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGT
GATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAA
CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC
CTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGT
GCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA
TCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTA
TCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAA
ATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAG
TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCC
CATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAG
TTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA
GTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCA
TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
ACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAA
TGCTGAT

SEQ ID NO. 6010
STRAIN 1169NT
ATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC
GGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
ATTAAGTAAGGAGGGTAAGCATTTGAAGGCGGATATTTTCTtTGGAGGAA
ATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCA
AAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC
GACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAG
CTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTA
AAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTC
ACAACTCACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAAG
CGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAAATCT
TCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAAATGATTGT
GGGGTTGACTTACGAAGACCCTAGTGTCAATTtGCAAAAAAGTGGTGCCA
ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCG
GTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTAT
TAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA
GTAACCGACCTATTCGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCT
TTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCA
TAAGGGCCAAATCCTTAAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6011
STRAIN JM91130013
CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACTCACCAATATACTCTTGGCAAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GGCAAAATGATTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTA
ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
TATGTCACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTCG
TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2{*} April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

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                             1                                                   50
      msa523010.2{263_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa523010.2{263_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa523010.2{263_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa523010.2{263_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa523010.2{263_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa523010.2{263_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa523010.2{263_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa523010.2{263_2603}  atgaaagaaa aacagtcgaa aaggcttatt tatatactac tggttgtttc
    msa523010.2{263_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa523010.2{263_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa523010.2{263_JM91130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus  ********** ********** ********** ********** **********

                             51                                                 100
      msa523010.2{263_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
      msa523010.2{263_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
      msa523010.2{263_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
      msa523010.2{263_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
      msa523010.2{263_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~taaac
       msa523010.2{263_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
    msa523010.2{263_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
      msa523010.2{263_2603}  cattattttt ataagtgttt ttacatacag tattagccag ccttctaaac
    msa523010.2{263_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag cctttaaac
    msa523010.2{263_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa523010.2{263_JM91130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~cag ccttctaaac
                  Consensus  ********** ********** ********** *******--- ----------

                             101                                                150
      msa523010.2{263_COH1}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
      msa523010.2{263_M732}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
      msa523010.2{263_M781}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
      msa523010.2{263_A909}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
      msa523010.2{263_H36B}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
       msa523010.2{263_090}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
    msa523010.2{263_18RS21}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
      msa523010.2{263_2603}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
    msa523010.2{263_CJB110}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
    msa523010.2{263_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~ATAG TCAAGCCATT
msa523010.2{263_JM91130013}  tacttccacc aaaagaatta gttattctaa gtccaaATAG TCAAGCCATT
                  Consensus  ---------- ---------- ---------- ------**** **********

                             151                                                200
      msa523010.2{263_COH1}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
      msa523010.2{263_M732}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
      msa523010.2{263_M781}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
      msa523010.2{263_A909}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
      msa523010.2{263_H36B}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
       msa523010.2{263_090}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
    msa523010.2{263_18RS21}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
      msa523010.2{263_2603}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
    msa523010.2{263_CJB110}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
    msa523010.2{263_1169NT}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
msa523010.2{263_JM91130013}  TTAACAGGAA CGATTCCAGC TTTTGAGGAA AAATACGGTA TAAAAGTTAA
                  Consensus  ********** ********** ********** ********** **********

                             201                                                250
      msa523010.2{263_COH1}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
      msa523010.2{263_M732}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
      msa523010.2{263_M781}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
      msa523010.2{263_A909}  GCTTATTCAA GGTGGGACAG GtCAACTAAT AGATAGATTA AGTAAGGAGG
      msa523010.2{263_H36B}  GCTTATTCAA GGTGGGACAG GtCAACTAAT AGATAGATTA AGTAAGGAGG
       msa523010.2{263_090}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
    msa523010.2{263_18RS21}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
      msa523010.2{263_2603}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
    msa523010.2{263_CJB110}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
    msa523010.2{263_1169NT}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
msa523010.2{263_JM91130013}  GCTTATTCAA GGTGGGACAG GgCAACTAAT AGATAGATTA AGTAAGGAGG
                  Consensus  ********** ********** *-******** ********** **********

                             251                                                300
      msa523010.2{263_COH1}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
      msa523010.2{263_M732}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
      msa523010.2{263_M781}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
      msa523010.2{263_A909}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
      msa523010.2{263_H36B}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
       msa523010.2{263_090}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
    msa523010.2{263_18RS21}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
      msa523010.2{263_2603}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
    msa523010.2{263_CJB110}  GTAAGCAgTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
    msa523010.2{263_1169NT}  GTAAGCAtTT GAAGGCGGAT aTTTTCTTTG GAGGAAATTA TACGCAATTT
msa523010.2{263_JM91130013}  GTAAGCAgTT GAAGGCGGAT gTTTTCTTTG GAGGAAATTA TACGCAATTT
                  Consensus  *******-** ********** -********* ********** **********
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Table 60: Comparative Sequences relating to SAG1945

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                                  301                                                  350
          msa523010.2{263_COH1}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
          msa523010.2{263_M732}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
          msa523010.2{263_M781}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
          msa523010.2{263_A909}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATaTTCATAC
          msa523010.2{263_H36B}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATaTTCATAC
           msa523010.2{263_090}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
        msa523010.2{263_18RS21}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
          msa523010.2{263_2603}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
        msa523010.2{263_CJB110}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
        msa523010.2{263_1169NT}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
    msa523010.2{263_JM9113O013}   GAAAGTCATA AGGCATTGTT TGAGTCTTAC GTATCAAAGA ATgTTCATAC
                      Consensus   ********** ********** ********** ********** **_*******

                                  351                                                  400
          msa523010.2{263_COH1}   TGTTATTCCA GAcTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
          msa523010.2{263_M732}   TGTTATTCCA GAcTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
          msa523010.2{263_M781}   TGTTATTCCA GAcTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
          msa523010.2{263_A909}   TGTTATTCCA GAtTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
          msa523010.2{263_H36B}   TGTTATTCCA GAtTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
           msa523010.2{263_090}   TGTTATTCCA GAcTATATCC ATCCaAGTGA TACGGCGACA CCTTATACTA
        msa523010.2{263_18RS21}   TGTTATTCCA GAcTATATCC ATCCaAGTGA TACGGCGACA CCTTATACTA
          msa523010.2{263_2603}   TGTTATTCCA GAcTATATCC ATCCaAGTGA TACGGCGACA CCTTATACTA
        msa523010.2{263_CJB110}   TGTTATTCCA GAcTATATCC ATCCaAGTGA TACGGCGACA CCTTATACTA
        msa523010.2{263_1169NT}   TGTTATTCCA GAcTATATCC ATCCaAGTGA TACGGCGACA CCTTATACTA
    msa523010.2{263_JM9113O013}   TGTTATTCCA GAcTATATCC ATCCgAGTGA TACGGCGACA CCTTATACTA
                      Consensus   ********** **_******* ****_***** ********** **********

                                  401                                                  450
          msa523010.2{263_COH1}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
          msa523010.2{263_M732}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
          msa523010.2{263_M781}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
          msa523010.2{263_A909}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
          msa523010.2{263_H36B}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGtTAA GGGACTTACC
           msa523010.2{263_090}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
        msa523010.2{263_18RS21}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
          msa523010.2{263_2603}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
        msa523010.2{263_CJB110}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
        msa523010.2{263_1169NT}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
    msa523010.2{263_JM9113O013}   TAAATGGGAG TGTCTTGATT GTAAATAACG AATTAGcTAA GGGACTTACC
                      Consensus   ********** ********** ********** ******_*** **********

                                  451                                                  500
          msa523010.2{263_COH1}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
          msa523010.2{263_M732}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
          msa523010.2{263_M781}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
          msa523010.2{263_A909}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
          msa523010.2{263_H36B}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
           msa523010.2{263_090}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
        msa523010.2{263_18RS21}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
          msa523010.2{263_2603}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
        msa523010.2{263_CJB110}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
        msa523010.2{263_1169NT}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
    msa523010.2{263_JM9113O013}   ATCAAGAGTT ATGAAGATTT ATTACAGCCT TCCTTAAAAG GTAAAATTGC
                      Consensus   ********** ********** ********** ********** **********

                                  501                                                  550
          msa523010.2{263_COH1}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
          msa523010.2{263_M732}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
          msa523010.2{263_M781}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
          msa523010.2{263_A909}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
          msa523010.2{263_H36B}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
           msa523010.2{263_090}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
        msa523010.2{263_18RS21}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
          msa523010.2{263_2603}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
        msa523010.2{263_CJB110}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACtAATA
        msa523010.2{263_1169NT}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACcAATA
    msa523010.2{263_JM9113O013}   CTTTGCAGAT CCGAATACTT CCTCTAGTGC TTTCTCACAA CTCACcAATA
                      Consensus   ********** ********** ********** ********** *****_****

                                  551                                                  600
          msa523010.2{263_COH1}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
          msa523010.2{263_M732}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
          msa523010.2{263_M781}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
          msa523010.2{263_A909}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
          msa523010.2{263_H36B}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
           msa523010.2{263_090}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
        msa523010.2{263_18RS21}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
          msa523010.2{263_2603}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
        msa523010.2{263_CJB110}   TACTCTTGGC cAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
        msa523010.2{263_1169NT}   TACTCTTGGC aAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
    msa523010.2{263_JM9113O013}   TACTCTTGGC aAAGGGTGGT TACACCAATC CAAAAGCGTG GAACTATGTT
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Table 60: Comparative Sequences relating to SAG1945

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                      Consensus  ********** -********* ********** ********** **********

                                 601                                              650
        msa523010.2{263_COH1}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
        msa523010.2{263_M732}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
        msa523010.2{263_M781}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
        msa523010.2{263_A909}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
        msa523010.2{263_H36B}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
         msa523010.2{263_090}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
      msa523010.2{263_18RS21}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
        msa523010.2{263_2603}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
      msa523010.2{263_CJB110}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
      msa523010.2{263_1169NT}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
  msa523010.2{263_JM9130013}    AAAAAGCTAC AACATAATAT TAATGCTATC AAATCTTCTA GCTCTTCAGA
                      Consensus  ********** ********** ********** ********** **********

                                 651                                              700
        msa523010.2{263_COH1}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
        msa523010.2{263_M732}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
        msa523010.2{263_M781}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
        msa523010.2{263_A909}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
        msa523010.2{263_H36B}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
         msa523010.2{263_090}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG cTGACTTACG
      msa523010.2{263_18RS21}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG cTGACTTACG
        msa523010.2{263_2603}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG cTGACTTACG
      msa523010.2{263_CJB110}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG cTGACTTACG
      msa523010.2{263_1169NT}    AGTTTATCAA TCAGTTGCAG AAGGaAAAAT GATTGTGGGG tTGACTTACG
  msa523010.2{263_JM9130013}    AGTTTATCAA TCAGTTGCAG AAGGcAAAAT GATTGTGGGG cTGACTTACG
                      Consensus  ********** ********** ****-***** ********** -*********

                                 701                                              750
        msa523010.2{263_COH1}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
        msa523010.2{263_M732}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
        msa523010.2{263_M781}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
        msa523010.2{263_A909}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
        msa523010.2{263_H36B}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
         msa523010.2{263_090}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
      msa523010.2{263_18RS21}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
        msa523010.2{263_2603}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
      msa523010.2{263_CJB110}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
      msa523010.2{263_1169NT}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTa
  msa523010.2{263_JM9130013}    AAGACCCTAG TGTCAATTTG CAAAAAAGTG GTGCCAATGT TTCTATTGTg
                      Consensus  ********** ********** ********** ********** *********-

                                 751                                              800
        msa523010.2{263_COH1}    TAcCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
        msa523010.2{263_M732}    TAcCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
        msa523010.2{263_M781}    TAcCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
        msa523010.2{263_A909}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
        msa523010.2{263_H36B}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
         msa523010.2{263_090}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
      msa523010.2{263_18RS21}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
        msa523010.2{263_2603}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
      msa523010.2{263_CJB110}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
      msa523010.2{263_1169NT}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
  msa523010.2{263_JM9130013}    TAtCCGACAG AAGGGACAGT TTTTGTCCCA TCTTCGGTTG CAATTATAAA
                      Consensus  **-******* ********** ********** ********** **********

                                 801                                              850
        msa523010.2{263_COH1}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
        msa523010.2{263_M732}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
        msa523010.2{263_M781}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
        msa523010.2{263_A909}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
        msa523010.2{263_H36B}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
         msa523010.2{263_090}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
      msa523010.2{263_18RS21}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
        msa523010.2{263_2603}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
      msa523010.2{263_CJB110}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
      msa523010.2{263_1169NT}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
  msa523010.2{263_JM9130013}    GAATGCTCCT TCTATGAAAG AAGCAAAGTT ATTTATTAAT TTTATGCTTT
                      Consensus  ********** ********** ********** ********** **********

                                 851                                              900
        msa523010.2{263_COH1}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
        msa523010.2{263_M732}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
        msa523010.2{263_M781}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
        msa523010.2{263_A909}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
        msa523010.2{263_H36B}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
         msa523010.2{263_090}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
      msa523010.2{263_18RS21}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
        msa523010.2{263_2603}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
      msa523010.2{263_CJB110}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
      msa523010.2{263_1169NT}    CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
```

Table 60: Comparative Sequences relating to SAG1945

```
msa523010.2{263_JM91130013}  CTTTAGATGT TCAAAATGCC TTTGGGCAGT CAACGAGTAA CCGACCTATT
                  Consensus  ********** ********** ********** ********** **********

                             901                                              950
        msa523010.2{263_COH1}  CGTAAAGATG CCCAAACaAG TAATGGCATG AAAGCTTTAA AGGATATcGC
        msa523010.2{263_M732}  CGTAAAGATG CCCAAACaAG TAATGGCATG AAAGCTTTAA AGGATATcGC
        msa523010.2{263_M781}  CGTAAAGATG CCCAAACaAG TAATGGCATG AAAGCTTTAA AGGATATcGC
        msa523010.2{263_A909}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
        msa523010.2{263_H36B}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
         msa523010.2{263_090}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
      msa523010.2{263_18RS21}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
        msa523010.2{263_2603}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
      msa523010.2{263_CJB110}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
      msa523010.2{263_1169NT}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
  msa523010.2{263_JM91130013}  CGTAAAGATG CCCAAACgAG TAATGGCATG AAAGCTTTAA AGGATATtGC
                    Consensus  ********** *******-** ********** ********** *******-**

                             951                                             1000
        msa523010.2{263_COH1}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG aGCCAAATCC
        msa523010.2{263_M732}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG aGCCAAATCC
        msa523010.2{263_M781}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG aGCCAAATCC
        msa523010.2{263_A909}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
        msa523010.2{263_H36B}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
         msa523010.2{263_090}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
      msa523010.2{263_18RS21}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
        msa523010.2{263_2603}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
      msa523010.2{263_CJB110}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
      msa523010.2{263_1169NT}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
  msa523010.2{263_JM91130013}  TACTCTTAAA GAAGATTATC GCTATGTCAC TAAGCATAAG gGCCAAATCC
                    Consensus  ********** ********** ********** ********** -*********

                             1001                            1035
        msa523010.2{263_COH1}  TTAAAACCTA TAATCGcATT CGTAGAAATG CTGAT
        msa523010.2{263_M732}  TTAAAACCTA TAATCGcATT CGTAGAAATG CTGAT
        msa523010.2{263_M781}  TTAAAACCTA TAATCGcATT CGTAGAAATG CTGAT
        msa523010.2{263_A909}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
        msa523010.2{263_H36B}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
         msa523010.2{263_090}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
      msa523010.2{263_18RS21}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
        msa523010.2{263_2603}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
      msa523010.2{263_CJB110}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
      msa523010.2{263_1169NT}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
  msa523010.2{263_JM91130013}  TTAAAACCTA TAATCGtATT CGTAGAAATG CTGAT
                    Consensus  ********** ******-*** ********** *****
```

SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVVSIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE
KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ
LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEGKMIVGLTYEDPSVNL
QKSGANVSIVYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLSLDVQNAFGQSTSNRPI
RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF
FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK
SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINAIKS
SSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNAPSM
KEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ
ILKTYNRIRRNAD

SEQ ID NO. 6016

Table 60: Comparative Sequences relating to SAG1945

STRAIN 18RS21 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6017
STRAIN M732 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6018
STRAIN COH1 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6019
STRAIN M781 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6020
STRAIN CJB110 frame: 1
QPFKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6021
STRAIN 1169NT frame: 3
SQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
FESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKI
AFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEGK
MIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNAPSMKEAKLFINFMLSLD
VQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6022
STRAIN JM91130013 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DVFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

```
PRETTY of: /biotmp/msa523117.2{*}   April 28, 2003 08:56  ..

                                1                                                50
       msa523117.2{263_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
       msa523117.2{263_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
       msa523117.2{263_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
     msa523117.2{263_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~SQAI
     msa523117.2{263_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pfkllppkel vilspnSQAI
        msa523117.2{263_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
     msa523117.2{263_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
       msa523117.2{263_2603}   mkekqskrli yillvvsiif isvftysisq pskllppkel vilspnSQAI
       msa523117.2{263_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
 msa523117.2{263_JM91130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~q pskllppkel vilspnSQAI
       msa523117.2{263_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~kllppkel vilspnSQAI
                   Consensus   ********** ********** *********- ---------- ------****

                                51                                              100
       msa523117.2{263_COH1}   LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
       msa523117.2{263_M732}   LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
       msa523117.2{263_M781}   LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
     msa523117.2{263_1169NT}   LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKhLKAD iFFGGNYTQF
```

Table 60: Comparative Sequences relating to SAG1945

```
    msa523117.2{263_CJB110}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
       msa523117.2{263_090}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
     msa523117.2{263_18RS21}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
      msa523117.2{263_2603}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
      msa523117.2{263_A909}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
 msa523117.2{263_JM91130013}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD vFFGGNYTQF
      msa523117.2{263_H36B}  LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF
                  Consensus  ********** ********** ********** *****_**** _*********

                             101                                                150
      msa523117.2{263_COH1}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
      msa523117.2{263_M732}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
      msa523117.2{263_M781}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
    msa523117.2{263_1169NT}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
    msa523117.2{263_CJB110}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
       msa523117.2{263_090}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
    msa523117.2{263_18RS21}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
      msa523117.2{263_2603}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
      msa523117.2{263_A909}  ESHKALFESY VSKNiHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
msa523117.2{263_JM91130013}  ESHKALFESY VSKNvHTVIP DYIHPSDTAT PYTINGSVLI VNNELaKGLT
      msa523117.2{263_H36B}  ESHKALFESY VSKNiHTVIP DYIHPSDTAT PYTINGSVLI VNNELvKGLT
                  Consensus  ********** ****_***** ********** ********** *****_****

                             151                                                200
      msa523117.2{263_COH1}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
      msa523117.2{263_M732}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
      msa523117.2{263_M781}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
    msa523117.2{263_1169NT}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
    msa523117.2{263_CJB110}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
       msa523117.2{263_090}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
    msa523117.2{263_18RS21}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
      msa523117.2{263_2603}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
      msa523117.2{263_A909}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
msa523117.2{263_JM91130013}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
      msa523117.2{263_H36B}  IKSYEDLLQP SLKGKIAFAD PNTSSSAFSQ LTNILLAKGG YTNPKAWNYV
                  Consensus  ********** ********** ********** ********** **********

                             201                                                250
      msa523117.2{263_COH1}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
      msa523117.2{263_M732}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
      msa523117.2{263_M781}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
    msa523117.2{263_1169NT}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
    msa523117.2{263_CJB110}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
       msa523117.2{263_090}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
    msa523117.2{263_18RS21}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
      msa523117.2{263_2603}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
      msa523117.2{263_A909}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
msa523117.2{263_JM91130013}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
      msa523117.2{263_H36B}  KKLQHNINAI KSSSSSEVYQ SVAEGKMIVG LTYEDPSVNL QKSGANVSIV
                  Consensus  ********** ********** ********** ********** **********

                             251                                                300
      msa523117.2{263_COH1}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
      msa523117.2{263_M732}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
      msa523117.2{263_M781}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
    msa523117.2{263_1169NT}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
    msa523117.2{263_CJB110}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
       msa523117.2{263_090}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
    msa523117.2{263_18RS21}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
      msa523117.2{263_2603}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
      msa523117.2{263_A909}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
msa523117.2{263_JM91130013}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
      msa523117.2{263_H36B}  YPTEGTVFVP SSVAIIKNAP SMKEAKLFIN FMLSLDVQNA FGQSTSNRPI
                  Consensus  ********** ********** ********** ********** **********

                             301                                     345
      msa523117.2{263_COH1}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK sQILKTYNRI RRNAD
      msa523117.2{263_M732}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK sQILKTYNRI RRNAD
      msa523117.2{263_M781}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK sQILKTYNRI RRNAD
    msa523117.2{263_1169NT}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
    msa523117.2{263_CJB110}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
       msa523117.2{263_090}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
    msa523117.2{263_18RS21}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
      msa523117.2{263_2603}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
      msa523117.2{263_A909}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
msa523117.2{263_JM91130013}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
      msa523117.2{263_H36B}  RKDAQTSNGM KALKDIATLK EDYRYVTKHK gQILKTYNRI RRNAD
                  Consensus  ********** ********** ********** _********* *****
```

Table 61: Comparative Sequences relating to SAG1030

SEQ ID NO. 6101
STRAIN 2603
ATGGTAAAAGTTAGTGTAAGTTCTGTAGGAACTCAAGCATCAACAGTAGCTATTTCTATG
TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT
CCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA
CAAACCTTATATGTCTCAATTTGTGGTGATGAGGATTTAGACTCTGTCGTTTTAGAATCA
AAATTAGCAAGTGATAGGGCATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAAC
GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCAT
TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAAACCGGAGCTTTTGGAAAACCAACA
TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCC
AAAGCTGAAGAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAAAGCGGCTAAT
GAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTATGAATCAATTATCAGTGGTTTA
AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT
CGGCTATTGATG

SEQ ID NO. 6102
STRAIN 090
TTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
AACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGA
GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT
GAGGATTTAGACTCTGTCGTTTTAGAATCAAAATTAGCAAGTGATAGGGC
ATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCAG
AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATT
TAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT
AGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
AAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAAG
AACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA
AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTATG
AATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG
GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103
STRAIN 18RS21
TTAAATGATGCAATAACAAAACTATCATCTTTTGCAGAGGC
TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTG
AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGA
TGAGGATTTAGACTCTGTCGTTTTAGAATCAAAATTAGCAAGTGATAGGG
CATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCA
GAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATT
AAAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
TTAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCA
ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
TAGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
CAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAAGCTGAA
GAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGA
AAATACTACTAAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAA
AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTAT
GAATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGA
GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

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PRETTY of: /biotmp/msa185066.2{*}   May 13, 2003 07:01  ..

                          1                                                50
  msa185066.2{270_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa185066.2{270_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa185066.2{270_2603}    atggtaaaag ttagtgtaag ttctgtagga actcaagcat caacagtagc
             Consensus    ********** ********** ********** ********** **********

                          51                                              100
  msa185066.2{270_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~TT AAATGATGCA ATAACAAAAC
msa185066.2{270_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~TT AAATGATGCA ATAACAAAAC
 msa185066.2{270_2603}    tatttctatg tttagtcgtg tatcggctTT AAATGATGCA ATAACAAAAC
             Consensus    ********** ********** ********** ********** **********

                          101                                             150
  msa185066.2{270_090}    TATCATCTTT TGCAGAGGCT GCAACTCTTC AAGGGACTGC TTATTCAAAT
msa185066.2{270_18RS21}   TATCATCTTT TGCAGAGGCT GCAACTCTTC AAGGGACTGC TTATTCAAAT
 msa185066.2{270_2603}    TATCATCTTT TGCAGAGGCT GCAACTCTTC AAGGGACTGC TTATTCAAAT
             Consensus    ********** ********** ********** ********** **********

                          151                                             200
  msa185066.2{270_090}    GCAAAAAGCT ATGCTACTGG AACGTTAACT CCGATGCTTC AAGGAATGAT
msa185066.2{270_18RS21}   GCAAAAAGCT ATGCTACTGG AACGTTAACT CCGATGCTTC AAGGAATGAT
 msa185066.2{270_2603}    GCAAAAAGCT ATGCTACTGG AACGTTAACT CCGATGCTTC AAGGAATGAT
```

Table 61: Comparative Sequences relating to SAG1030

```
               Consensus  ********** ********** ********** ********** **********

                          201                                                250
   msa185066.2{270_090}   TCTTTTCTCT GAAACATTGA GTGAGAAATG TACAGAATTA CAAACCTTAT
 msa185066.2{270_18RS21}  TCTTTTCTCT GAAACATTGA GTGAGAAATG TACAGAATTA CAAACCTTAT
  msa185066.2{270_2603}   TCTTTTCTCT GAAACATTGA GTGAGAAATG TACAGAATTA CAAACCTTAT
               Consensus  ********** ********** ********** ********** **********

                          251                                                300
   msa185066.2{270_090}   ATGTCTCAAT TTGTGGTGAT GAGGATTTAG ACTCTGTCGT TTTAGAATCA
 msa185066.2{270_18RS21}  ATGTCTCAAT TTGTGGTGAT GAGGATTTAG ACTCTGTCGT TTTAGAATCA
  msa185066.2{270_2603}   ATGTCTCAAT TTGTGGTGAT GAGGATTTAG ACTCTGTCGT TTTAGAATCA
               Consensus  ********** ********** ********** ********** **********

                          301                                                350
   msa185066.2{270_090}   AAATTAGCAA GTGATAGGGC ATCATTAAAG ATTGCTGAAG CACTTTTAGA
 msa185066.2{270_18RS21}  AAATTAGCAA GTGATAGGGC ATCATTAAAG ATTGCTGAAG CACTTTTAGA
  msa185066.2{270_2603}   AAATTAGCAA GTGATAGGGC ATCATTAAAG ATTGCTGAAG CACTTTTAGA
               Consensus  ********** ********** ********** ********** **********

                          351                                                400
   msa185066.2{270_090}   GCATCTTAAC GATGATCCAG AACCTTCCAA ATCTGCCATA AGTTCTACAA
 msa185066.2{270_18RS21}  GCATCTTAAC GATGATCCAG AACCTTCCAA ATCTGCCATA AGTTCTACAA
  msa185066.2{270_2603}   GCATCTTAAC GATGATCCAG AACCTTCCAA ATCTGCCATA AGTTCTACAA
               Consensus  ********** ********** ********** ********** **********

                          401                                                450
   msa185066.2{270_090}   AAAGTAATAT TAAAAAATTA AAAAAACGTA TAAAATCTAA TCAAAAGAAA
 msa185066.2{270_18RS21}  AAAGTAATAT TAAAAAATTA AAAAAACGTA TAAAATCTAA TCAAAAGAAA
  msa185066.2{270_2603}   AAAGTAATAT TAAAAAATTA AAAAAACGTA TAAAATCTAA TCAAAAGAAA
               Consensus  ********** ********** ********** ********** **********

                          451                                                500
   msa185066.2{270_090}   TTAGACAACC TTAATGAATT TAACGCCCAT TCAGCAACAG TATTTGCGGA
 msa185066.2{270_18RS21}  TTAGACAACC TTAATGAATT TAACGCCCAT TCAGCAACAG TATTTGCGGA
  msa185066.2{270_2603}   TTAGACAACC TTAATGAATT TAACGCCCAT TCAGCAACAG TATTTGCGGA
               Consensus  ********** ********** ********** ********** **********

                          501                                                550
   msa185066.2{270_090}   CATTTCTAAT GCACAGTCAA CTGTTAACCA AGCACTAGCG GCTGTTTCAA
 msa185066.2{270_18RS21}  CATTTCTAAT GCACAGTCAA CTGTTAACCA AGCACTAGCG GCTGTTTCAA
  msa185066.2{270_2603}   CATTTCTAAT GCACAGTCAA CTGTTAACCA AGCACTAGCG GCTGTTTCAA
               Consensus  ********** ********** ********** ********** **********

                          551                                                600
   msa185066.2{270_090}   CAGGATTTTC TGGATATAAT AGTAAAACCG GAGCTTTTGG AAAACCAACA
 msa185066.2{270_18RS21}  CAGGATTTTC TGGATATAAT AGTAAAACCG GAGCTTTTGG AAAACCAACA
  msa185066.2{270_2603}   CAGGATTTTC TGGATATAAT AGTAAAACCG GAGCTTTTGG AAAACCAACA
               Consensus  ********** ********** ********** ********** **********

                          601                                                650
   msa185066.2{270_090}   TCCGGACAGA TGGAATGGAC AAAGACAGTT AAGAAGAATT GGAAAGAGCG
 msa185066.2{270_18RS21}  TCCGGACAGA TGGAATGGAC AAAGACAGTT AAGAAGAATT GGAAAGAGCG
  msa185066.2{270_2603}   TCCGGACAGA TGGAATGGAC AAAGACAGTT AAGAAGAATT GGAAAGAGCG
               Consensus  ********** ********** ********** ********** **********

                          651                                                700
   msa185066.2{270_090}   AGAAGACGCC AAAGCTGAAG AACTGAAAAG TAAAAAGGCT GAAGAAAGTA
 msa185066.2{270_18RS21}  AGAAGACGCC AAAGCTGAAG AACTGAAAAG TAAAAAGGCT GAAGAAAGTA
  msa185066.2{270_2603}   AGAAGACGCC AAAGCTGAAG AACTGAAAAG TAAAAAGGCT GAAGAAAGTA
               Consensus  ********** ********** ********** ********** **********

                          701                                                750
   msa185066.2{270_090}   AGAAAGCTTC AAAAATTGAA AATACTACTA AAAAAAGTAA TGTTTCAGTT
 msa185066.2{270_18RS21}  AGAAAGCTTC AAAAATTGAA AATACTACTA AAAAAAGTAA TGTTTCAGTT
  msa185066.2{270_2603}   AGAAAGCTTC AAAAATTGAA AATACTACTA AAAAAAGTAA TGTTTCAGTT
               Consensus  ********** ********** ********** ********** **********

                          751                                                800
   msa185066.2{270_090}   GATAAAAAGA AATTAATAAA AGCGGCTAAT GAAGCGTATA AATTAGGAGA
 msa185066.2{270_18RS21}  GATAAAAAGA AATTAATAAA AGCGGCTAAT GAAGCGTATA AATTAGGAGA
  msa185066.2{270_2603}   GATAAAAAGA AATTAATAAA AGCGGCTAAT GAAGCGTATA AATTAGGAGA
               Consensus  ********** ********** ********** ********** **********

                          801                                                850
   msa185066.2{270_090}   AATTAAAAAA GATACCTATG AATCAATTAT CAGTGGTTTA AGTAATGCAT
 msa185066.2{270_18RS21}  AATTAAAAAA GATACCTATG AATCAATTAT CAGTGGTTTA AGTAATGCAT
  msa185066.2{270_2603}   AATTAAAAAA GATACCTATG AATCAATTAT CAGTGGTTTA AGTAATGCAT
               Consensus  ********** ********** ********** ********** **********

                          851                                                900
   msa185066.2{270_090}   CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
 msa185066.2{270_18RS21}  CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
```

Table 61: Comparative Sequences relating to SAG1030

```
msa185066.2{270_2603}  CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
            Consensus  ********** ********** ********** ********** **********

                       901        912
  msa185066.2{270_090}  CGGCTATTGA TG
msa185066.2{270_18RS21}  CGGCTATTGA TG
 msa185066.2{270_2603}  CGGCTATTGA TG
             Consensus  ********** **
```

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSALNDAITKLSSFAEAATLQGTAYSNAKSYATGTLT
PMLQGMILFSETLSEKCTELQTLYVSICGDEDLDSVVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
NTTKKSNVSVDKKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLYVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIISGLSNASAALLKEVAKSKLTDTARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLYVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIISGLSNASAALLKEVAKSKLTDTARLLM

```
PRETTY of: /biotmp/msa185181.2{*}   May 13, 2003 07:03  ..

                         1                                                   50
  msa185181.2{270_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~LNDA ITKLSSFAEA ATLQGTAYSN
msa185181.2{270_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~LNDA ITKLSSFAEA ATLQGTAYSN
 msa185181.2{270_2603}  mvkvsvssvg tqastvaism fsrvsaLNDA ITKLSSFAEA ATLQGTAYSN
             Consensus  ********** ********** ********** ********** **********

                         51                                                 100
  msa185181.2{270_090}  AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLYVSICGD EDLDSVVLES
msa185181.2{270_18RS21}  AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLYVSICGD EDLDSVVLES
 msa185181.2{270_2603}  AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLYVSICGD EDLDSVVLES
             Consensus  ********** ********** ********** ********** **********

                         101                                                150
  msa185181.2{270_090}  KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_18RS21}  KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
 msa185181.2{270_2603}  KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
             Consensus  ********** ********** ********** ********** **********

                         151                                                200
  msa185181.2{270_090}  LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_18RS21}  LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
 msa185181.2{270_2603}  LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
             Consensus  ********** ********** ********** ********** **********

                         201                                                250
  msa185181.2{270_090}  SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKSNVSV
msa185181.2{270_18RS21}  SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKSNVSV
 msa185181.2{270_2603}  SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKSNVSV
             Consensus  ********** ********** ********** ********** **********

                         251                                                300
  msa185181.2{270_090}  DKKKLIKAAN EAYKLGEIKK DTYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_18RS21}  DKKKLIKAAN EAYKLGEIKK DTYESIISGL SNASAALLKE VAKSKLTDTA
 msa185181.2{270_2603}  DKKKLIKAAN EAYKLGEIKK DTYESIISGL SNASAALLKE VAKSKLTDTA
             Consensus  ********** ********** ********** ********** **********

                         301
  msa185181.2{270_090}  RLLM
msa185181.2{270_18RS21}  RLLM
 msa185181.2{270_2603}  RLLM
             Consensus  ****
```

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201
STRAIN 2603
ATGATTTTAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA
GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA
GCTTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATAT
AGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGC
CATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCA
GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGA
GACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGT
TTTAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
ATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTA
GTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGAC
TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6202
STRAIN 090
TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC
ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA
TAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAATACAATAGTTTTA
CTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAG
GATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGA
AACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAG
CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
GGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
CAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCAT
CTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGCTTTCATTTT
AATTaTCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCA
TCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATTTAGTTGCAT
GTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCTAAT
GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA
TGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6203
STRAIN A909
TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA
GGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA
ATGTGACGATAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAATACA
ATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACT
TTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATG
TACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAG
CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
AATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTG
GTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGC
TTTCATTTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTTTGA
TGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATT
TAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTT
GTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA
AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGG
AAAATAAA

SEQ ID NO. 6204
STRAIN H36B
TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA
CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
AAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTC
CCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTA
ACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAAT
TTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGAT
TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCG
TTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAA
CAGTAGCTTTTAAGCCAGGGGTCAGCTTTCATTTTAATTATCAAGATATC
ATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAA
AAATCAACTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAAC
ATTATCAAGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGA
GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA
AGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6205
STRAIN 18RS21
TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
CATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATATAG
AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG

Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6206
STRAIN M732
TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
CATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATATAG
AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
TTTCTTTGnCATTTGGAAAATAAA

SEQ ID NO. 6207
STRAIN COH1
TTGCTGGAT
TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC
TTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAAC
ATCTCCTCGCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTT
CCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGG
TATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTG
CAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT
AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
CCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATT
CTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAA
CAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTCAGTTTTCATTTTACTTA
TCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTG
CTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGTT
ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT
GAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGT
GGAATCAAAAAGTTTATGATTTTCTTTGGCATTTGGAAAATAAA

SEQ ID NO. 6208
STRAIN M781
TTGCTGGA
TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG
CTTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAA
CATCTCCTCGCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTT
TCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATG
GTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACT
GCAAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTT
TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG
ACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAAT
TCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGA
ACAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTCAGTTTTCATTTTACTT
ATCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCT
GCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGT
TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT
TGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAG
TGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209
STRAIN CJB110
TTGCTGGATTATCCTCGAATTAAGGC
GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA
AAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCACAAAAATT
GTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATATTCCCAAATA
TAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTG
ATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTTAAA
GAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT
ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG
ACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTA
ATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC
TTTTAAGCCAGGGGTCAGCTTTCATTTTAATTATCAAGATATCATCAATC
ATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAA
CTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCA
AGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGAGTTTATT
ATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTAT
GATTTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6210
STRAIN 1169NT
AATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTCATTTTTTAAAATACAATAGTTTTACTTTTCCCTATAT
TCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTT
TAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTA
ATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAG
ATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTT
AACAGTAGGTTTTAAGCCAGGGGTCAGCTTTCATTTTACTTATCAAGATA
TCATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATT
AAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCGTGTGTTATCCCAAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6211
STRAIN JM9130013
ATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAAAAATTGTTCATTTTTTAAAAT
ACAATAGTTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCT
ACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATAC
ATGTACGATTGAAACTGCAAAACTAATTTTTAAAGAAGGTAAAATCTTAT
CAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCATCTGaACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTC
AGCTTTCATTTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTT
TGATGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAAC
ATTTAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGC
CTTGTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAA
CGAAACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGGAAAATAAA

```
PRETTY of: /biotmp/msa185284.2{*}   May 13, 2003 07:08  ..

                              1                                                    50
       msa185284.2{271_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa185284.2{271_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa185284.2{271_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa185284.2{271_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_2603}   atgattttaa aaatttgtcg tgcagcatat agtttacaat ggggaggtgt
      msa185284.2{271_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa185284.2{271_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus   ********** ********** ********** ********** **********

                              51                                                  100
       msa185284.2{271_090}   ~~~~~~~~~~ ~~~~~~~tgg attatcctct aattaaggcg tttgaattgg
      msa185284.2{271_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~ttaaggcg tttgaattgg
 msa185284.2{271_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa185284.2{271_A909}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
    msa185284.2{271_CJB110}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
    msa185284.2{271_18RS21}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
      msa185284.2{271_2603}   ttaccaatta gctTTGCtgg attatcctcg aattaaggcg tttgaattgg
      msa185284.2{271_M732}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
      msa185284.2{271_M781}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
      msa185284.2{271_COH1}   ~~~~~~~~~~ ~~~TTGCtgg attatcctcg aattaaggcg tttgaattgg
    msa185284.2{271_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ aattaaggcg tttgaattgg
                  Consensus   ********** *******--- ---------- ---------- ----------

                              101                                                 150
       msa185284.2{271_090}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAtT
      msa185284.2{271_H36B}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAtT
 msa185284.2{271_JM9130013}   ~~~~~ATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAtT
      msa185284.2{271_A909}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAtT
    msa185284.2{271_CJB110}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAtT
    msa185284.2{271_18RS21}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
      msa185284.2{271_2603}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
      msa185284.2{271_M732}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
      msa185284.2{271_M781}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
      msa185284.2{271_COH1}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
    msa185284.2{271_1169NT}   aaaggATAGG AGCTTTCATA GCTTACGAGA AACAATATAA AAGAAAAAcT
                  Consensus   -----***** ********** ********** ********** ********-*

                              151                                                 200
       msa185284.2{271_090}   GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT
```

Table 62: Comparative Sequences relating to SAG0690

```
     msa185284.2{271_H36B}  GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT
msa185284.2{271_JM9130013}  GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT
     msa185284.2{271_A909}  GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT
   msa185284.2{271_CJB110}  GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT
   msa185284.2{271_18RS21}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
     msa185284.2{271_2603}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
     msa185284.2{271_M732}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
     msa185284.2{271_M781}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
     msa185284.2{271_COH1}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
   msa185284.2{271_1169NT}  GAGATACAAT GTGACGATAA ACATCTCCTC gCAAAAATTG TTCATTTTTT
                 Consensus  ********** ********** ********** _********* **********

                            201                                               250
      msa185284.2{271_090}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_H36B}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
msa185284.2{271_JM9130013}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_A909}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
   msa185284.2{271_CJB110}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
   msa185284.2{271_18RS21}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_2603}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_M732}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_M781}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
     msa185284.2{271_COH1}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
   msa185284.2{271_1169NT}  AAAATACAAT AGTTTTACTT TTCCCTATAT TCCCAAATAT AGAGAAGCGG
                 Consensus  ********** ********** ********** ********** **********

                            251                                               300
      msa185284.2{271_090}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_H36B}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
msa185284.2{271_JM9130013}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_A909}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
   msa185284.2{271_CJB110}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
   msa185284.2{271_18RS21}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_2603}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_M732}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_M781}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
     msa185284.2{271_COH1}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
   msa185284.2{271_1169NT}  CAGCTACTTT TAATGAGGAT GGTATTAGTT TAACTTCTGA TTTTTTAAGC
                 Consensus  ********** ********** ********** ********** **********

                            301                                               350
      msa185284.2{271_090}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_H36B}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
msa185284.2{271_JM9130013}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_A909}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
   msa185284.2{271_CJB110}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
   msa185284.2{271_18RS21}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_2603}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_M732}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_M781}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
     msa185284.2{271_COH1}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
   msa185284.2{271_1169NT}  CATACATGTA CGATTGAAAC TGCAAAACTA ATTTTTAAAG AAGGTAAAAT
                 Consensus  ********** ********** ********** ********** **********

                            351                                               400
      msa185284.2{271_090}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
     msa185284.2{271_H36B}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
msa185284.2{271_JM9130013}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
     msa185284.2{271_A909}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
   msa185284.2{271_CJB110}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
   msa185284.2{271_18RS21}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAaG
     msa185284.2{271_2603}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAaG
     msa185284.2{271_M732}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAaG
     msa185284.2{271_M781}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAaG
     msa185284.2{271_COH1}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAaG
   msa185284.2{271_1169NT}  CTTATCAGCA GTTAAAGCCT TTAATAAGCC TGCTGAAGTA CTGGTAAAtG
                 Consensus  ********** ********** ********** ********** ********_*

                            401                                               450
      msa185284.2{271_090}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_H36B}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
msa185284.2{271_JM9130013}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_A909}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
   msa185284.2{271_CJB110}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
   msa185284.2{271_18RS21}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_2603}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_M732}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_M781}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
     msa185284.2{271_COH1}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
   msa185284.2{271_1169NT}  ATAAGAGGAA TGCTGCTGGA GACCCTAAAG ATTACTTTGA CTATGTGATG
                 Consensus  ********** ********** ********** ********** **********

                            451                                               500
```

Table 62: Comparative Sequences relating to SAG0690

```
        msa185284.2{271_090}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_H36B}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
   msa185284.2{271_JM9130013} TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_A909}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
     msa185284.2{271_CJB110}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
     msa185284.2{271_18RS21}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_2603}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_M732}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_M781}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
       msa185284.2{271_COH1}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
     msa185284.2{271_1169NT}  TTGAACTGGT CAAATACCAA TTCTGGTTAT CGTTTAGTAA TGGAAAGATT
                   Consensus  ********** ********** ********** ********** **********

                              501                                              550
        msa185284.2{271_090}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGcT TTTAAGCCAG
       msa185284.2{271_H36B}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGcT TTTAAGCCAG
   msa185284.2{271_JM9130013} GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGcT TTTAAGCCAG
       msa185284.2{271_A909}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGcT TTTAAGCCAG
     msa185284.2{271_CJB110}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGcT TTTAAGCCAG
     msa185284.2{271_18RS21}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
       msa185284.2{271_2603}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
       msa185284.2{271_M732}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
       msa185284.2{271_M781}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
       msa185284.2{271_COH1}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
     msa185284.2{271_1169NT}  GTTAGGCAAA GCACCATCTG AACAGGAGTT AACAGTAGgT TTTAAGCCAG
                   Consensus  ********** ********** ********** ********_* **********

                              551                                              600
        msa185284.2{271_090}  GGGTCAGcTT TCATTTTAaT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_H36B}  GGGTCAGcTT TCATTTTAaT TATCAAGATA TCATCAATCA TCCTGATTCT
   msa185284.2{271_JM9130013} GGGTCAGcTT TCATTTTAaT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_A909}  GGGTCAGcTT TCATTTTAaT TATCAAGATA TCATCAATCA TCCTGATTCT
     msa185284.2{271_CJB110}  GGGTCAGcTT TCATTTTAaT TATCAAGATA TCATCAATCA TCCTGATTCT
     msa185284.2{271_18RS21}  GGGTCAGtTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_2603}  GGGTCAGtTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_M732}  GGGTCAGtTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_M781}  GGGTCAGtTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
       msa185284.2{271_COH1}  GGGTCAGtTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
     msa185284.2{271_1169NT}  GGGTCAGcTT TCATTTTAcT TATCAAGATA TCATCAATCA TCCTGATTCT
                   Consensus  *******_** ********_* ********** ********** **********

                              601                                              650
        msa185284.2{271_090}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAaC TTTCTTTAGC
       msa185284.2{271_H36B}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAaC TTTCTTTAGC
   msa185284.2{271_JM9130013} ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAaC TTTCTTTAGC
       msa185284.2{271_A909}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAaC TTTCTTTAGC
     msa185284.2{271_CJB110}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAaC TTTCTTTAGC
     msa185284.2{271_18RS21}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
       msa185284.2{271_2603}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
       msa185284.2{271_M732}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
       msa185284.2{271_M781}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
       msa185284.2{271_COH1}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
     msa185284.2{271_1169NT}  ATTTTTGATG GTTATCATCC TGCTAAAATT AAAAATCAgC TTTCTTTAGC
                   Consensus  ********** ********** ********** ********_* **********

                              651                                              700
        msa185284.2{271_090}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_H36B}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
   msa185284.2{271_JM9130013} AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_A909}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
     msa185284.2{271_CJB110}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
     msa185284.2{271_18RS21}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_2603}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_M732}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_M781}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
       msa185284.2{271_COH1}  AGAACATTTA GTTGCaTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
     msa185284.2{271_1169NT}  AGAACATTTA GTTGCgTGTG TTATCCCAAA ACATTATCAA GAAGATTATC
                   Consensus  ********** *****_**** ********** ********** **********

                              701                                              750
        msa185284.2{271_090}  AAAgcCTTGT GCCtAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
       msa185284.2{271_H36B}  AAAgcCTTGT GCCtAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
   msa185284.2{271_JM9130013} AAAgcCTTGT GCCtAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
       msa185284.2{271_A909}  AAAgcCTTGT GCCtAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
     msa185284.2{271_CJB110}  AAAgcCTTGT GCCtAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
     msa185284.2{271_18RS21}  AAAgcCTTGT GCCcAATGAC TTGAAACACA GgGTTTATTA TTTAGATTAC
       msa185284.2{271_2603}  AAAgcCTTGT GCCcAATGAC TTGAAACACA GgGTTTATTA TTTAGATTAC
       msa185284.2{271_M732}  AAAgcCTTGT GCCcAATGAC TTGAAACACA GgGTTTATTA TTTAGATTAC
       msa185284.2{271_M781}  AAAgcCTTGT GCCcAATGAC TTGAAACACA GgGTTTATTA TTTAGATTAC
       msa185284.2{271_COH1}  AAAgcCTTGT GCCcAATGAC TTGAAACACA GgGTTTATTA TTTAGATTAC
     msa185284.2{271_1169NT}  AAAatCTTGT GCCcAATGAC TTGAAACACA GaGTTTATTA TTTAGATTAC
                   Consensus  ***__***** ***_****** ********** *_******** **********
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Table 62: Comparative Sequences relating to SAG0690

```
                                751                                                   800
         msa185284.2{271_090}   TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_H36B}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
     msa185284.2{271_JM9130013} TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_A909}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
       msa185284.2{271_CJB110}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
       msa185284.2{271_18RS21}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_2603}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_M732}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_M781}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
         msa185284.2{271_COH1}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
       msa185284.2{271_1169NT}  TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG
                    Consensus   ********** ********** ********** ********** **********

                                801        816
         msa185284.2{271_090}   tCATTTGGAA AATAAA
         msa185284.2{271_H36B}  tCATTTGGAA AATAAA
     msa185284.2{271_JM9130013} tCATTTGGAA AATAAA
         msa185284.2{271_A909}  tCATTTGGAA AATAAA
       msa185284.2{271_CJB110}  tCATTTGGAA AATAAA
       msa185284.2{271_18RS21}  tCATTTGGAA AATAAA
         msa185284.2{271_2603}  tCATTTGGAA AATAAA
         msa185284.2{271_M732}  nCATTTGGAA AATAAA
         msa185284.2{271_M781}  tCATTTGGAA AATAAA
         msa185284.2{271_COH1}  gCATTTGGAA AATAAA
       msa185284.2{271_1169NT}  tCATTTGGAA AATAAA
                    Consensus   -********* ******
```

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSLQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLL
AKIVHFLKYNSFTFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA
VKAFNKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG
FKPGVSFHFTYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND
LKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREAAATFN
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPA
KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCH
LENK

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLXHLENK

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLWHLENK

SEQ ID NO. 6218

STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSFTFPYIPKYREAAATF
NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFD
YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSIFDGYHP
AKIKNQLSLAEHLVACVIPKHYQEDYQNLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC
HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREAAATFNEDGISLT
SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDYVMLNWSN
TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPAKIKNQLS
LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSFTFPYIPKYREA
AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPK
DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFD
GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVY
DFLCHLENK

```
PRETTY of: /biotmp/msa185358.2{*}   May 13, 2003 07:11  ..

                                1                                                   50
       msa185358.2{271_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~dyplika felerIGAFI AYEKQYKRKi
  msa185358.2{271_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~IGAFI AYEKQYKRKi
      msa185358.2{271_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~ka felerIGAFI AYEKQYKRKi
      msa185358.2{271_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKi
    msa185358.2{271_CJB110}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKi
    msa185358.2{271_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~ika felerIGAFI AYEKQYKRKt
    msa185358.2{271_18RS21}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKt
      msa185358.2{271_2603}    milkicraay slqwggvyql aLLdyprika felerIGAFI AYEKQYKRKt
      msa185358.2{271_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKt
      msa185358.2{271_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKt
      msa185358.2{271_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~LLdyprika felerIGAFI AYEKQYKRKt
                  Consensus    ********** ********** ***------- -----***** *********-

                                51                                                 100
       msa185358.2{271_090}    EIQCDDKHLL tKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
  msa185358.2{271_JM9130013}   EIQCDDKHLL tKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_H36B}    EIQCDDKHLL tKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_A909}    EIQCDDKHLL tKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
    msa185358.2{271_CJB110}    EIQCDDKHLL tKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
    msa185358.2{271_1169NT}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
    msa185358.2{271_18RS21}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_2603}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_M732}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_M781}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
      msa185358.2{271_COH1}    EIQCDDKHLL aKIVHFLKYN SFTFPYIPKY REAAATFNED GISLTSDFLS
                  Consensus    ********** -********* ********** ********** **********

                                101                                                150
       msa185358.2{271_090}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
  msa185358.2{271_JM9130013}   HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
      msa185358.2{271_H36B}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
      msa185358.2{271_A909}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
    msa185358.2{271_CJB110}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
    msa185358.2{271_1169NT}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVnDKRNAAG DPKDYFDYVM
    msa185358.2{271_18RS21}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVkDKRNAAG DPKDYFDYVM
      msa185358.2{271_2603}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVkDKRNAAG DPKDYFDYVM
      msa185358.2{271_M732}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVkDKRNAAG DPKDYFDYVM
      msa185358.2{271_M781}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVkDKRNAAG DPKDYFDYVM
      msa185358.2{271_COH1}    HTCTIETAKL IFKEGKILSA VKAFNKPAEV LVkDKRNAAG DPKDYFDYVM
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Table 62: Comparative Sequences relating to SAG0690

```
                 Consensus  ********** ********** ********** **_******* **********

                            151                                                200
        msa185358.2{271_090}  LNWSNTNSGY RLVMERLLGK APSEQELTVa FKPGVSFHFn YQDIINHPDS
   msa185358.2{271_JM9130013}  LNWSNTNSGY RLVMERLLGK APSEQELTVa FKPGVSFHFn YQDIINHPDS
       msa185358.2{271_H36B}  LNWSNTNSGY RLVMERLLGK APSEQELTVa FKPGVSFHFn YQDIINHPDS
       msa185358.2{271_A909}  LNWSNTNSGY RLVMERLLGK APSEQELTVa FKPGVSFHFn YQDIINHPDS
     msa185358.2{271_CJB110}  LNWSNTNSGY RLVMERLLGK APSEQELTVa FKPGVSFHFn YQDIINHPDS
     msa185358.2{271_1169NT}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
     msa185358.2{271_18RS21}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
       msa185358.2{271_2603}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
       msa185358.2{271_M732}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
       msa185358.2{271_M781}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
       msa185358.2{271_COH1}  LNWSNTNSGY RLVMERLLGK APSEQELTVg FKPGVSFHFt YQDIINHPDS
                  Consensus  ********** ********** *********_ *********_ **********

                            201                                                250
        msa185358.2{271_090}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
   msa185358.2{271_JM9130013}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_H36B}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_A909}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
     msa185358.2{271_CJB110}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
     msa185358.2{271_1169NT}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQnLVPND LKHRVYYLDY
     msa185358.2{271_18RS21}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_2603}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_M732}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_M781}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
       msa185358.2{271_COH1}  IFDGYHPAKI KNQLSLAEHL VACVIPKHYQ EDYQsLVPND LKHRVYYLDY
                  Consensus  ********** ********** ********** ****_***** **********

                            251                  272
        msa185358.2{271_090}  CNETLYEWNQ KVYDFLcHLE NK
   msa185358.2{271_JM9130013}  CNETLYEWNQ KVYDFLcHLE NK
       msa185358.2{271_H36B}  CNETLYEWNQ KVYDFLcHLE NK
       msa185358.2{271_A909}  CNETLYEWNQ KVYDFLcHLE NK
     msa185358.2{271_CJB110}  CNETLYEWNQ KVYDFLcHLE NK
     msa185358.2{271_1169NT}  CNETLYEWNQ KVYDFLcHLE NK
     msa185358.2{271_18RS21}  CNETLYEWNQ KVYDFLcHLE NK
       msa185358.2{271_2603}  CNETLYEWNQ KVYDFLcHLE NK
       msa185358.2{271_M732}  CNETLYEWNQ KVYDFLxHLE NK
       msa185358.2{271_M781}  CNETLYEWNQ KVYDFLcHLE NK
       msa185358.2{271_COH1}  CNETLYEWNQ KVYDFLwHLE NK
                  Consensus  ********** ******_*** **
```

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6301
STRAIN 2603
ATGAAAAGTCGAAAAAAAGATAAATTGGTATTGAGGTTAACAACAACACTATTGGTTTTT
GGTTTGGGTGGGGTTTGGTTTTATAATTATAAAAATGATAATGTCGAACCGACAGTCACT
AGTGCATCGGATCAAACGACGACTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATT
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCC
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT
CAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
GAGTTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG
GATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
AACCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302
STRAIN 090
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303
STRAIN A909
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6304
STRAIN H36B
GGGGTTTGGTTTTATAATTATAAAAATGATA
ATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
CAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTA
TGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAAT
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGG
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTaTGCATCT
GCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAAC
AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305
STRAIN 18RS21
GGGGTTTGGTTTTATAATTATAAAAATGATAATG
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGC
GTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAG
ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATAT
AAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAA
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTT
TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGG
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTG
AAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306
STRAIN M732
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6307
STRAIN COH1
GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308
STRAIN M781
GGGGTTTGGTTTTATAATTATAAAAATGA
TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA
TTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTG
TATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACA
ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG
AATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAA
GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC
TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCAT
CTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTA
ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAAT
TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309
STRAIN CJB110
GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310
STRAIN 1169NT
GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACAGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311
STRAIN JM9130013
TTTGGTTTTATAATTATAAAAATGATAATGTCGAACCGACAGTCACTAGT
GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT
TGAAATTTCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAG
CTATTTTGGAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAAATCTGTTCAAAT
GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG
TTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTC
TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG
CTTATGCTAGTAAATTAAACCAAATTATTGAAAACTACAGTCTAGATGCT
TATGATAAA

```
PRETTY of: /biotmp/msa243324.2{*}   February 11, 2003 05:11  ..

                                1                                                    50
      msa243324.2{275_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa243324.2{275_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa243324.2{275_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa243324.2{275_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa243324.2{275_2603}   atgaaaagtc gaaaaaaaga taaattggta ttgaggttaa caacaacact
    msa243324.2{275_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa243324.2{275_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa243324.2{275_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
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Table 63: Comparative Sequences relating to SAG1912

```
      msa243324.2{275_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa243324.2{275_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa243324.2{275_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus  ********** ********** ********** ********** **********

                             51                                                100
      msa243324.2{275_A909}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
      msa243324.2{275_H36B}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
       msa243324.2{275_090}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
     msa243324.2{275_18RS21}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
      msa243324.2{275_2603}  attggttttt ggtttgggtg gggTTTGGTT TTATAATTAT AAAAATGATA
     msa243324.2{275_CJB110}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
      msa243324.2{275_COH1}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
      msa243324.2{275_M732}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
      msa243324.2{275_M781}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
    msa243324.2{275_1169NT}  ~~~~~~~~~~ ~~~~~~~~~g gggTTTGGTT TTATAATTAT AAAAATGATA
  msa243324.2{275_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~TTTGGTT TTATAATTAT AAAAATGATA
                  Consensus  ********** *********- ---******* ********** **********

                             101                                               150
      msa243324.2{275_A909}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
      msa243324.2{275_H36B}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
       msa243324.2{275_090}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
     msa243324.2{275_18RS21}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
      msa243324.2{275_2603}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
     msa243324.2{275_CJB110}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
      msa243324.2{275_COH1}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
      msa243324.2{275_M732}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
      msa243324.2{275_M781}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
    msa243324.2{275_1169NT}  ATGTCGAACa GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
  msa243324.2{275_JM9130013}  ATGTCGAACc GACAGTCACT AGTGCATCGG ATCAAACGAC GACTTTTATT
                  Consensus  *********- ********** ********** ********** **********

                             151                                               200
      msa243324.2{275_A909}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
      msa243324.2{275_H36B}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
       msa243324.2{275_090}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
     msa243324.2{275_18RS21}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
      msa243324.2{275_2603}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
     msa243324.2{275_CJB110}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
      msa243324.2{275_COH1}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
      msa243324.2{275_M732}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
      msa243324.2{275_M781}  CAAACGATTT CtCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
    msa243324.2{275_1169NT}  CAAACGATTT CcCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
  msa243324.2{275_JM9130013}  CAAACGATTT CcCCAACAGC TATTGAAATT TCTAAGACCT ATGATTTGTA
                  Consensus  ********** *-******** ********** ********** **********

                             201                                               250
      msa243324.2{275_A909}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
      msa243324.2{275_H36B}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
       msa243324.2{275_090}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
     msa243324.2{275_18RS21}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
      msa243324.2{275_2603}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
     msa243324.2{275_CJB110}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
      msa243324.2{275_COH1}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
      msa243324.2{275_M732}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
      msa243324.2{275_M781}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
    msa243324.2{275_1169NT}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
  msa243324.2{275_JM9130013}  TGCGTCAGTC TTATTAGCAC AAGCTATTTT GGAATCATCC AGTGGACAAT
                  Consensus  ********** ********** ********** ********** **********

                             251                                               300
      msa243324.2{275_A909}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
      msa243324.2{275_H36B}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
       msa243324.2{275_090}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
     msa243324.2{275_18RS21}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
      msa243324.2{275_2603}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
     msa243324.2{275_CJB110}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
      msa243324.2{275_COH1}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
      msa243324.2{275_M732}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
      msa243324.2{275_M781}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
    msa243324.2{275_1169NT}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
  msa243324.2{275_JM9130013}  CAGATTTGTC TAAGGCTCCT AATTATAACC TCTTTGGCAT CAAAGGAGAA
                  Consensus  ********** ********** ********** ********** **********

                             301                                               350
      msa243324.2{275_A909}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
      msa243324.2{275_H36B}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
       msa243324.2{275_090}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
     msa243324.2{275_18RS21}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
      msa243324.2{275_2603}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
     msa243324.2{275_CJB110}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
      msa243324.2{275_COH1}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
```

Table 63: Comparative Sequences relating to SAG1912

```
     msa243324.2{275_M732}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
     msa243324.2{275_M781}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
   msa243324.2{275_1169NT}  TATAAAGGTA AATCTGTcCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
msa243324.2{275_JM9130013}  TATAAAGGTA AATCTGTtCA AATGCCTACT TTAGAAGATG ATGGGAAAGG
                 Consensus  ********** *******-** ********** ********** **********

                            351                                                400
     msa243324.2{275_A909}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
     msa243324.2{275_H36B}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
      msa243324.2{275_090}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
   msa243324.2{275_18RS21}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
     msa243324.2{275_2603}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
   msa243324.2{275_CJB110}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
     msa243324.2{275_COH1}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
     msa243324.2{275_M732}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
     msa243324.2{275_M781}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
   msa243324.2{275_1169NT}  cAATATGACt CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
msa243324.2{275_JM9130013}  tAATATGACc CAAATCCAAG CTCCTTTTCG CGCCTATCCA AATTATTCTG
                 Consensus  -********- ********** ********** ********** **********

                            401                                                450
     msa243324.2{275_A909}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
     msa243324.2{275_H36B}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
      msa243324.2{275_090}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
   msa243324.2{275_18RS21}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
     msa243324.2{275_2603}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
   msa243324.2{275_CJB110}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
     msa243324.2{275_COH1}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
     msa243324.2{275_M732}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
     msa243324.2{275_M781}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
   msa243324.2{275_1169NT}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
msa243324.2{275_JM9130013}  CTTCACTATA TGATTATGCT GAGTTAGTAT CTAGTCAAAA GTATGCATCT
                 Consensus  ********** ********** ********** ********** **********

                            451                                                500
     msa243324.2{275_A909}  GcTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
     msa243324.2{275_H36B}  GcTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
      msa243324.2{275_090}  GtTTGGAAAT CAAATACcTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
   msa243324.2{275_18RS21}  GtTTGGAAAT CAAATACcTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
     msa243324.2{275_2603}  GtTTGGAAAT CAAATACcTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
   msa243324.2{275_CJB110}  GtTTGGAAAT CAAATACcTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
     msa243324.2{275_COH1}  GtTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
     msa243324.2{275_M732}  GtTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
     msa243324.2{275_M781}  GtTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
   msa243324.2{275_1169NT}  GtTTGGAAAT CAAATACtTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
msa243324.2{275_JM9130013}  GtTTGGAAAT CAAATACcTC TTCTTATAAG GATGCTACTG CAGCTCTAAC
                 Consensus  *-******** *******-** ********** ********** **********

                            501                                                550
     msa243324.2{275_A909}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
     msa243324.2{275_H36B}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
      msa243324.2{275_090}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
   msa243324.2{275_18RS21}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
     msa243324.2{275_2603}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
   msa243324.2{275_CJB110}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
     msa243324.2{275_COH1}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
     msa243324.2{275_M732}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
     msa243324.2{275_M781}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
   msa243324.2{275_1169NT}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
msa243324.2{275_JM9130013}  AGGTCTTTAT GCGACAGATA CTGCTTATGC TAGTAAATTA AACCAAATTA
                 Consensus  ********** ********** ********** ********** **********

                            551                          582
     msa243324.2{275_A909}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
     msa243324.2{275_H36B}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
      msa243324.2{275_090}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
   msa243324.2{275_18RS21}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
     msa243324.2{275_2603}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
   msa243324.2{275_CJB110}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
     msa243324.2{275_COH1}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
     msa243324.2{275_M732}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
     msa243324.2{275_M781}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
   msa243324.2{275_1169NT}  TTGAAAcCTA CAGTCTAGAT GCTTATGATA AA
msa243324.2{275_JM9130013}  TTGAAAaCTA CAGTCTAGAT GCTTATGATA AA
                 Consensus  ******-*** ********** ********** **
```

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKKDKLVLRLTTTLLVFGLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEI
SKTYDLYASVLLAQAILESSSGQSDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMT
QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKL
NQIIETYSLDAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313
STRAIN 090 frame: 1 .
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314
STRAIN A909 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315
STRAIN H36B frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316
STRAIN 18RS21 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317
STRAIN M732 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318
STRAIN M781 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319
STRAIN CJB110 frame: 1
GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320
STRAIN 1169NT frame: 1
GVWFYNYKNDNVEQTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321
STRAIN JM9130013 frame: 3
WFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQSD
LSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

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PRETTY of: /biotmp/msa243476.2{*}   February 11, 2003 05:17  ..

                             1                                                50
      msa243476.2{275_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
    msa243476.2{275_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
     msa243476.2{275_2603}   mksrkkdklv lrltttllvf glggvWFYNY KNDNVEpTVT SASDQTTTFI
    msa243476.2{275_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
     msa243476.2{275_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
     msa243476.2{275_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
     msa243476.2{275_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
     msa243476.2{275_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEpTVT SASDQTTTFI
 msa243476.2{275_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~WFYNY KNDNVEpTVT SASDQTTTFI
   msa243476.2{275_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~gvWFYNY KNDNVEqTVT SASDQTTTFI
                 Consensus   ********** ********** ***--***** ******-*** **********

                             51                                              100
      msa243476.2{275_090}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
    msa243476.2{275_18RS21}  QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
     msa243476.2{275_2603}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
    msa243476.2{275_CJB110}  QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
     msa243476.2{275_M732}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
     msa243476.2{275_M781}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
     msa243476.2{275_A909}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
     msa243476.2{275_H36B}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
 msa243476.2{275_JM9130013}  QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
   msa243476.2{275_1169NT}   QTISPTAIEI SKTYDLYASV LLAQAILESS SGQSDLSKAP NYNLFGIKGE
                 Consensus   ********** ********** ********** ********** **********
```

Table 63: Comparative Sequences relating to SAG1912

```
                             101                                                150
       msa243476.2{275_090}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
     msa243476.2{275_18RS21} YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
      msa243476.2{275_2603}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
     msa243476.2{275_CJB110} YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
      msa243476.2{275_M732}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
      msa243476.2{275_M781}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
      msa243476.2{275_A909}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
      msa243476.2{275_H36B}  YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
   msa243476.2{275_JM9130013} YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
     msa243476.2{275_1169NT} YKGKSVQMPT LEDDGKGNMT QIQAPFRAYP NYSASLYDYA ELVSSQKYAS
                   Consensus ********** ********** ********** ********** **********

                             151                                     194
       msa243476.2{275_090}  vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
     msa243476.2{275_18RS21} vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
      msa243476.2{275_2603}  vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
     msa243476.2{275_CJB110} vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
      msa243476.2{275_M732}  vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
      msa243476.2{275_M781}  vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
      msa243476.2{275_A909}  aWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
      msa243476.2{275_H36B}  aWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
   msa243476.2{275_JM9130013} vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEnYSLD AYDK
     msa243476.2{275_1169NT} vWKSNTSSYK DATAALTGLY ATDTAYASKL NQIIEtYSLD AYDK
                   Consensus -********* ********** ********** *****-**** ****
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Table 64: Comparative Sequences relating to SAG 0827

SEQ ID NO. 6401
STRAIN 2603
ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
ATGCTTCCAAATTCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTT
GGCCCTTTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
ATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAAA
CTTCTAGGAGTTCTAGATTTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATG
TTTGGAGTTGAAAAG

SEQ ID NO. 6402
STRAIN 090
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATA

SEQ ID NO. 6403
STRAIN A909
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTAT
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTC
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG
TGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
ATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTA
CCTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTC
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG
TAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTT
GAAAAG

SEQ ID NO. 6404
STRAIN H36B
CTCTATTCTCAGATGAAACAAATGCTCTTGC
CAACTTATCAAATGCTTCAGCTATGCTAAaTGCTATGCTTCCAAATTCTG
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCT
TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTG
TGGTGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
AGCATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTA
GTACCTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTC
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT
TTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGA
GTTGAAAAG

SEQ ID NO. 6405
STRAIN 18RS21
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCT
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6406
STRAIN M732
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6407
STRAIN COH1
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAAC
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATT
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTC
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA
TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC
CCATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTG
AAAAG

SEQ ID NO. 6408
STRAIN M781
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6409
STRAIN CJB110
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6410
STRAIN 1169NT
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCCA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6411
STRAIN JM9130013
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

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PRETTY of: /biotmp/msa236796.2{*}   February 11, 2003 02:42  ..

                               1                                                  50
      msa236796.2{282_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa236796.2{282_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa236796.2{282_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa236796.2{282_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa236796.2{282_CJB110}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa236796.2{282_18RS21}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa236796.2{282_2603}    atgaacaagt ctaagaaaat cgaaaattat caattattat tactacaagc
      msa236796.2{282_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa236796.2{282_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa236796.2{282_JM9130013}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa236796.2{282_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus    ********** ********** ********** ********** **********

                               51                                                100
      msa236796.2{282_COH1}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
      msa236796.2{282_M732}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
      msa236796.2{282_M781}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
       msa236796.2{282_090}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
    msa236796.2{282_CJB110}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
    msa236796.2{282_18RS21}    ~~~~~CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
      msa236796.2{282_2603}    gcaagCTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
```

Table 64: Comparative Sequences relating to SAG 0827

```
      msa236796.2{282_A909}  -----CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
      msa236796.2{282_H36B}  -----CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
 msa236796.2{282_JM9130013}  -----CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
    msa236796.2{282_1169NT}  -----CTCTA TTCTCAGATG AAACAAATGC TCTTGCCAAC TTATCAAATG
                  Consensus  ********** ********** ********** ********** **********

                             101                                              150
      msa236796.2{282_COH1}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
      msa236796.2{282_M732}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
      msa236796.2{282_M781}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
       msa236796.2{282_090}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
    msa236796.2{282_CJB110}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
    msa236796.2{282_18RS21}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
      msa236796.2{282_2603}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
      msa236796.2{282_A909}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
      msa236796.2{282_H36B}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
 msa236796.2{282_JM9130013}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
    msa236796.2{282_1169NT}  CTTCAGCTAT GCTAAATGCT ATGCTTCCAA ATTCTGTATT TACAGGCTTT
                  Consensus  ********** ********** ********** ********** **********

                             151                                              200
      msa236796.2{282_COH1}  TATTTATTTG ATGGAgAgGA GTTAATTCTT GGCCCTTTtC AGGGTGGTGT
      msa236796.2{282_M732}  TATTTATTTG ATGGAgAgGA GTTAATTCTT GGCCCTTTtC AGGGTGGTGT
      msa236796.2{282_M781}  TATTTATTTG ATGGAgAgGA GTTAATTCTT GGCCCTTTtC AGGGTGGTGT
       msa236796.2{282_090}  TATTTATTTG ATGGAaAgGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
    msa236796.2{282_CJB110}  TATTTATTTG ATGGAaAgGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
    msa236796.2{282_18RS21}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
      msa236796.2{282_2603}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
      msa236796.2{282_A909}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
      msa236796.2{282_H36B}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
 msa236796.2{282_JM9130013}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
    msa236796.2{282_1169NT}  TATTTATTTG ATGGAgAaGA GTTAATTCTT GGCCCTTTcC AGGGTGGTGT
                  Consensus  ********** *****-*-** ********** ********-* **********

                             201                                              250
      msa236796.2{282_COH1}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
      msa236796.2{282_M732}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
      msa236796.2{282_M781}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
       msa236796.2{282_090}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
    msa236796.2{282_CJB110}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
    msa236796.2{282_18RS21}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
      msa236796.2{282_2603}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
      msa236796.2{282_A909}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
      msa236796.2{282_H36B}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
 msa236796.2{282_JM9130013}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
    msa236796.2{282_1169NT}  ATCATGTGTG CATATTACTT TAGGAAAAGG TGTTTGTGGT GAATCTGCAC
                  Consensus  ********** ********** ********** ********** **********

                             251                                              300
      msa236796.2{282_COH1}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
      msa236796.2{282_M732}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
      msa236796.2{282_M781}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
       msa236796.2{282_090}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
    msa236796.2{282_CJB110}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
    msa236796.2{282_18RS21}  AAACTGCTAA GACGCTGATc GTTGATGATG TTACAAAGCA TGCTAACTAT
      msa236796.2{282_2603}  AAACTGCTAA GACGCTGATc GTTGATGATG TTACAAAGCA TGCTAACTAT
      msa236796.2{282_A909}  AAACTGCTAA GACGCTGATc GTTGATGATG TTACAAAGCA TGCTAACTAT
      msa236796.2{282_H36B}  AAACTGCTAA GACGCTGATc GTTGATGATG TTACAAAGCA TGCTAACTAT
 msa236796.2{282_JM9130013}  AAACTGCTAA GACGCTGATc GTTGATGATG TTACAAAGCA TGCTAACTAT
    msa236796.2{282_1169NT}  AAACTGCTAA GACGCTGATt GTTGATGATG TTACAAAGCA TGCTAACTAT
                  Consensus  ********** *********- ********** ********** **********

                             301                                              350
      msa236796.2{282_COH1}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CcATGTTTAA
      msa236796.2{282_M732}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CcATGTTTAA
      msa236796.2{282_M781}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CcATGTTTAA
       msa236796.2{282_090}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
    msa236796.2{282_CJB110}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
    msa236796.2{282_18RS21}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
      msa236796.2{282_2603}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
      msa236796.2{282_A909}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
      msa236796.2{282_H36B}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
 msa236796.2{282_JM9130013}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CtATGTTTAA
    msa236796.2{282_1169NT}  ATCTCCTGTG ATTCAAAAGC TATGAGTGAA ATCGTAGTAC CcATGTTTAA
                  Consensus  ********** ********** ********** ********** *-********

                             351                                              400
      msa236796.2{282_COH1}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
      msa236796.2{282_M732}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
      msa236796.2{282_M781}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
       msa236796.2{282_090}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
    msa236796.2{282_CJB110}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
    msa236796.2{282_18RS21}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
```

Table 64: Comparative Sequences relating to SAG 0827

```
     msa236796.2{282_2603}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
     msa236796.2{282_A909}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
     msa236796.2{282_H36B}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
msa236796.2{282_JM9130013}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
   msa236796.2{282_1169NT}  AAATGGCAAA CTTCTAGGAG TTCTAGATTT AGATTCTTCT TTAGTAGCAG
                 Consensus  ********** ********** ********** ********** **********

                            401                                                450
     msa236796.2{282_COH1}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
     msa236796.2{282_M732}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
     msa236796.2{282_M781}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
      msa236796.2{282_090}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
   msa236796.2{282_CJB110}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
   msa236796.2{282_18RS21}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
     msa236796.2{282_2603}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
     msa236796.2{282_A909}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
     msa236796.2{282_H36B}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
msa236796.2{282_JM9130013}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
   msa236796.2{282_1169NT}  ATTATGATGA GATTGATCAA GAATACTTAG AAAAATTTGT AGGTATTCTA
                 Consensus  ********** ********** ********** ********** **********

                            451                                           495
     msa236796.2{282_COH1}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
     msa236796.2{282_M732}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
     msa236796.2{282_M781}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
      msa236796.2{282_090}  GTAGAACATA CGATTTGGAA TTTGGATA-- ---------- -----
   msa236796.2{282_CJB110}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
   msa236796.2{282_18RS21}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
     msa236796.2{282_2603}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
     msa236796.2{282_A909}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
     msa236796.2{282_H36B}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
msa236796.2{282_JM9130013}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
   msa236796.2{282_1169NT}  GTAGAACATA CGATTTGGAA TTTGGATAtg tttggagttg aaaag
                 Consensus  ********** ********** ********-- ---------- -----
```

SEQ ID NO. 6412
STRAIN 2603 frame: 1
MNKSKKIENYQLLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELIL
GPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGK
LLGVLDLDSSLVADYDEIDQEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6413
STRAIN 090 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLD

SEQ ID NO. 6414
STRAIN A909 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6415
STRAIN H36B frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6416
STRAIN 18RS21 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6417
STRAIN M732 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6418
STRAIN COH1 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6419
STRAIN M781 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6420
STRAIN M781 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6421
STRAIN CJB110 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6422
STRAIN 1169NT frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

SEQ ID NO. 6423
STRAIN JM9130013 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEELILGPFQGGVSCVHITLGKGVC
GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSSLVADYDEID
QEYLEKFVGILVEHTIWNLDMFGVEK

```
PRETTY of: /biotmp/msa237960.2{*}   February 11, 2003 02:46  ..

                                1                                                   50
     msa237960.2{282_1169NT}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
      msa237960.2{282_18RS21}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_2603}   mnkskkieny qllllqaqaL FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_A909}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_COH1}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_H36B}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
   msa237960.2{282_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_M732}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
        msa237960.2{282_M781}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
         msa237960.2{282_090}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
      msa237960.2{282_CJB110}   ~~~~~~~~~~ ~~~~~~~~~L FSDETNALAN LSNASAMLNA MLPNSVFTGF
                    Consensus   ********** ********** ********** ********** **********

                                51                                                 100
      msa237960.2{282_1169NT}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
      msa237960.2{282_18RS21}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_2603}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_A909}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_COH1}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_H36B}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
   msa237960.2{282_JM9130013}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_M732}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
        msa237960.2{282_M781}   YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
         msa237960.2{282_090}   YLFDGkELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
      msa237960.2{282_CJB110}   YLFDGkELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
                    Consensus   *****-**** ********** ********** ********** **********

                                101                                                150
      msa237960.2{282_1169NT}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
      msa237960.2{282_18RS21}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_2603}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_A909}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_COH1}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_H36B}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
   msa237960.2{282_JM9130013}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_M732}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
        msa237960.2{282_M781}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
         msa237960.2{282_090}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
      msa237960.2{282_CJB110}   ISCDSKAMSE IVVPMFKNGK LLGVLDLDSS LVADYDEIDQ EYLEKFVGIL
                    Consensus   ********** ********** ********** ********** **********

                                151         165
      msa237960.2{282_1169NT}   VEHTIWNLDm fgvek
      msa237960.2{282_18RS21}   VEHTIWNLDm fgvek
        msa237960.2{282_2603}   VEHTIWNLDm fgvek
        msa237960.2{282_A909}   VEHTIWNLDm fgvek
        msa237960.2{282_COH1}   VEHTIWNLDm fgvek
        msa237960.2{282_H36B}   VEHTIWNLDm fgvek
   msa237960.2{282_JM9130013}   VEHTIWNLDm fgvek
        msa237960.2{282_M732}   VEHTIWNLDm fgvek
        msa237960.2{282_M781}   VEHTIWNLDm fgvek
         msa237960.2{282_090}   VEHTIWNLD~ ~~~~~
      msa237960.2{282_CJB110}   VEHTIWNLDm fgvek
                    Consensus   *********- -----
```

Table 65: Comparative Sequences relating to SAG0231

SEQ ID NO. 6501
STRAIN 2603
ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA
TTATTCATACTTGTTTTTAGCGGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG
AATATAGAAGAAATAAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
TGTACTGTAAAGATTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
TTGGAATCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6502
STRAIN 090
GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACA
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAAATTATAGCGGAAATTTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTC
AGAtGGtCAGGAGAAGATaCAA

SEQ ID NO. 6503
STRAIN A909
GGAGGATTTTATATGAAAGAACAACAA
AGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA
AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATC
CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCA
TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC
GAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTG
ATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGAT
GGtCAGGAGAAGATACAA

SEQ ID NO. 6504
STRAIN H36B
GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACA
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTAtTTTTTC
AGATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6505
STRAIN 18RS21
GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAG
ATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6506
STRAIN M781
GGAGGATTTTATATGAAAGAACAACAAAGAAAA
GAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
GAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCTGTTT
CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAAT
GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA
AAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAA
GAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAG
GAGAAGATACAA

SEQ ID NO. 6507
STRAIN CJB110
GGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA
TTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCTGTTTCAACTG
AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAATGATAAA
AAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAAATTA
TAGCGGAAATTTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAATTG
GTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6508
STRAIN 1169NT
GGAGGATTTTATATGAAAGAACAACAAAG
AAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG
CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATT
TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
AAAAAAATTATAGTGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAGATGG
TCAGGAGAAGATACAA

SEQ ID NO. 6509
STRAIN JM9130013
GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAAAACTATAAAAATTATTTTTTCAG
AtGGtCAGGAGAAGATACAA

```
PRETTY of: /biotmp/msa75400.2{*}   March 10, 2003 09:56  ..

                               1                                                   50
      msa75400.2{286_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa75400.2{286_CJB110}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa75400.2{286_18RS21}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa75400.2{286_2603}    atgaaaaaga gtacccaaat aatactacta atagttgcat tattcatact
     msa75400.2{286_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa75400.2{286_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa75400.2{286_JM9130013}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa75400.2{286_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa75400.2{286_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus    ********** ********** ********** ********** **********

                             51                                                 100
      msa75400.2{286_090}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
   msa75400.2{286_CJB110}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
   msa75400.2{286_18RS21}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
     msa75400.2{286_2603}    tgtttttagc GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
     msa75400.2{286_A909}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
     msa75400.2{286_H36B}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_JM9130013}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
     msa75400.2{286_M781}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
   msa75400.2{286_1169NT}    ~~~~~~~~~~ GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
                Consensus    ********** ********** ********** ********** **********

                             101                                                150
      msa75400.2{286_090}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
   msa75400.2{286_CJB110}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
   msa75400.2{286_18RS21}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
     msa75400.2{286_2603}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
     msa75400.2{286_A909}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
     msa75400.2{286_H36B}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
msa75400.2{286_JM9130013}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
     msa75400.2{286_M781}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
   msa75400.2{286_1169NT}    TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC ATTGAAAAAT
                Consensus    ********** ********** ********** ********** **********

                             151                                                200
      msa75400.2{286_090}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
   msa75400.2{286_CJB110}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
   msa75400.2{286_18RS21}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
     msa75400.2{286_2603}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
     msa75400.2{286_A909}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
     msa75400.2{286_H36B}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_JM9130013}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
     msa75400.2{286_M781}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
   msa75400.2{286_1169NT}    TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
                Consensus    ********** ********** ********** ********** **********

                             201                                                250
      msa75400.2{286_090}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
   msa75400.2{286_CJB110}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
   msa75400.2{286_18RS21}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
     msa75400.2{286_2603}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
     msa75400.2{286_A909}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
     msa75400.2{286_H36B}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
msa75400.2{286_JM9130013}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
     msa75400.2{286_M781}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
   msa75400.2{286_1169NT}    AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCATTT AATGATAAAA
                Consensus    ********** ********** ********** ********** **********

                             251                                                300
      msa75400.2{286_090}    AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
   msa75400.2{286_CJB110}    AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
   msa75400.2{286_18RS21}    AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
```

Table 65: Comparative Sequences relating to SAG0231

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     msa75400.2{286_2603}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
     msa75400.2{286_A909}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
     msa75400.2{286_H36B}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_JM9130013}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
     msa75400.2{286_M781}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
   msa75400.2{286_1169NT}  AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
                Consensus  ********** ********** ********** ********** **********

                           301                                                350
      msa75400.2{286_090}  AGcGGAAAtT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
   msa75400.2{286_CJB110}  AGcGGAAAtT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
   msa75400.2{286_18RS21}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
     msa75400.2{286_2603}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
     msa75400.2{286_A909}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
     msa75400.2{286_H36B}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
msa75400.2{286_JM9130013}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
     msa75400.2{286_M781}  AGcGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
   msa75400.2{286_1169NT}  AGtGGAAAaT TTAATGAAAA AAATATGAAT TTTTTTGATT CAAGAATTGG
                Consensus  **-*****-* ********** ********** ********** **********

                           351                                                400
      msa75400.2{286_090}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
   msa75400.2{286_CJB110}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
   msa75400.2{286_18RS21}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
     msa75400.2{286_2603}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
     msa75400.2{286_A909}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
     msa75400.2{286_H36B}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_JM9130013}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
     msa75400.2{286_M781}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
   msa75400.2{286_1169NT}  TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
                Consensus  ********** ********** ********** ********** **********

                           401
      msa75400.2{286_090}  TACAA
   msa75400.2{286_CJB110}  TACAA
   msa75400.2{286_18RS21}  TACAA
     msa75400.2{286_2603}  TACAA
     msa75400.2{286_A909}  TACAA
     msa75400.2{286_H36B}  TACAA
msa75400.2{286_JM9130013}  TACAA
     msa75400.2{286_M781}  TACAA
   msa75400.2{286_1169NT}  TACAA
                Consensus  *****
```

SEQ ID NO. 6510
STRAIN 2603 frame: 1
MKKSTQIILLIVALFILVFSGGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTK
KTIKIIFSDGQEKIQ

SEQ ID NO. 6511
STRAIN 090
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6512
STRAIN A909
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
CTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEK
IQ

SEQ ID NO. 6513
STRAIN H36B
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6514
STRAIN 18RS21
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQE
KIQ

SEQ ID NO. 6515
STRAIN CJB110
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
ISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6516
STRAIN JM9130013
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW

Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQE
KIQ

SEQ ID NO. 6517
STRAIN 1169NT frame: 1
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6518
STRAIN M781 frame: 1
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFFDSRIGKTKKTIKIIFSDGQEKIQ

```
PRETTY of: /biotmp/msa75376.2{*}    March 10, 2003 10:01  ..

                           1                                                50
      msa75376.2{286_090}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
   msa75376.2{286_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
   msa75376.2{286_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
     msa75376.2{286_2603}  mkkstqiill ivalfilvfs GGFYMKEQQR KEELKRNREY EVSLVKALKN
     msa75376.2{286_A909}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
   msa75376.2{286_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
     msa75376.2{286_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
     msa75376.2{286_M781}  ~~~~~~~~~~ ~~~~~~~~~~ GGFYMKEQQR KEELKRNREY EVSLVKALKN
                Consensus  ********** ********** ********** ********** **********

                           51                                              100
      msa75376.2{286_090}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
   msa75376.2{286_1169NT}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
   msa75376.2{286_18RS21}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
     msa75376.2{286_2603}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
     msa75376.2{286_A909}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
   msa75376.2{286_CJB110}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
     msa75376.2{286_H36B}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_JM9130013}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
     msa75376.2{286_M781}  SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
                Consensus  ********** ********** ********** ********** **********

                           101                                135
      msa75376.2{286_090}  SGnFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
   msa75376.2{286_1169NT}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
   msa75376.2{286_18RS21}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
     msa75376.2{286_2603}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
     msa75376.2{286_A909}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
   msa75376.2{286_CJB110}  SGnFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
     msa75376.2{286_H36B}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
msa75376.2{286_JM9130013}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
     msa75376.2{286_M781}  SGkFNEKNMN FFDSRIGKTK KTIKIIFSDG QEKIQ
                Consensus  **-******* ********** ********** *****
```

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6601
STRAIN 2603
TTGACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATG
GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAAGCAGCGCTT
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAG
GATCCTAGATTAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCAACTAGAT
GAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTCACAAAAATCAAATACCA
AAGTTAGTTTATATTTCAGCCAACAGCGGCTATTCAGCTTACATTAAAAGTAAAAGGAAG
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATG
TATGGTGAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGATAGTGGCA
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAA
TTAAATAATAAA

SEQ ID NO. 6602
STRAIN 090
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTA
TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6603
STRAIN A909
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC
ACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6604
STRAIN H36B
TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATGG
AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
TAAAGGTGATATATTTAAGGATCCTAGATTAACCTACATTAGGGGAGATA
TTACAGAAGCTGATAAGATTCATTTAGAAGACAGAACTTTTGATATATTA
ATTGACTGTATTGGAGCGATTAAGCCCAATCAACTAGATGAGCTTAACGT
TAAAGCAACCCAAAAAGCAGTAGCACTCTGTCACAAAAATCAAATACCAA
AGTTAGTTTATATTTCAGCCAACAGCGGCTATTCAGCTTACATTAAAAGT
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTTCC
AAGCCAAGTGTATAAAGTTATTTAGTCATTTGCCTTTCTTAGGTATTGTT
GTACAAAAGGTCTTTCCAACTAAGGTTGTGATAGTGGCAGAAGCAATCGT
TACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAAT
TAAATAATAAA

SEQ ID NO. 6605
STRAIN 18RS21
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTA
TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAAATaATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606
STRAIN M732
CAAAATGAAGGAGAgGGAACTATGgAAATACTGATTGCAGGTGGTAGTGG
TTTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGG
TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCcT
AGATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTT
AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGC
CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCA
CTCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAG
CGGCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCA
AAGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGT
GAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAG
TCATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGG
TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAAACCAACT
CAAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607
STRAIN COH1
ACAAGGCATATAAAAATTTCTATACTAAATTTAC
AAAATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGT
TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGT
GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA
GATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTA
GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCC
CAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCAC
TCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGC
GGCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAA
AGCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTG
AAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGT
CATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGT
TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAAACCAACTC
AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608
STRAIN M781
ACAAGGCATATAAAAATTTcTATACTAAATTTaCA
AAATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTT
TTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG
ATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAG
AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCC
AATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACT
CTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGCG
GCTATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAA
GCAAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGA
AGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTC
ATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGTT
GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAAACCAACTCA
AAAAATCCTTTCTAtTGAAGAATTAAATAATAAA

SEQ ID NO. 6609
STRAIN 1169NT
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAACAGCGGC
TATTCAGCTTACATTAGAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610
STRAIN CJB110
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGC
TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTCACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGC
TATTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAAACCAACCCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

```
SEQ ID NO. 6611
STRAIN JM9130013
ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC
ACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCtTTCTTAgGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
TCCTTTCTATTGAAGAATTAAATAATAAA

PRETTY of: /biotmp/msa137119.2{*}   April 10, 2003 03:30  ..

                              1                                                 50
      msa137119.2{303_COH1}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
      msa137119.2{303_M732}   ---------- ---------- ---------- ------CAAA ATGAAGGAGA
      msa137119.2{303_m781}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
       msa137119.2{303_090}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
    msa137119.2{303_18RS21}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
      msa137119.2{303_2603}   ttgacaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
      msa137119.2{303_A909}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
    msa137119.2{303_CJB110}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
      msa137119.2{303_H36B}   ---------- -tataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
 msa137119.2{303_JM9130013}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
    msa137119.2{303_1169NT}   ---acaaggc atataaaaat ttctatacta aatttaCAAA ATGAAGGAGA
                  Consensus   ***------- ---------- ---------- ------**** **********

                              51                                               100
      msa137119.2{303_COH1}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
      msa137119.2{303_M732}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
      msa137119.2{303_m781}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
       msa137119.2{303_090}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
    msa137119.2{303_18RS21}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
      msa137119.2{303_2603}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
      msa137119.2{303_A909}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
    msa137119.2{303_CJB110}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
      msa137119.2{303_H36B}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
 msa137119.2{303_JM9130013}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
    msa137119.2{303_1169NT}   GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaAAGC
                  Consensus   ********** ********** ********** ********** -****-****

                              101                                              150
      msa137119.2{303_COH1}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAggTGGC TTACTTATCA
      msa137119.2{303_M732}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAggTGGC TTACTTATCA
      msa137119.2{303_m781}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAggTGGC TTACTTATCA
       msa137119.2{303_090}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
    msa137119.2{303_18RS21}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
      msa137119.2{303_2603}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
      msa137119.2{303_A909}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
    msa137119.2{303_CJB110}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
      msa137119.2{303_H36B}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
 msa137119.2{303_JM9130013}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAagTGGC TTACTTATCA
    msa137119.2{303_1169NT}   AGATAATAAA AGCAGCGCTT ACAAAAGGGC ATAAgtTGGC TTACTTATCA
                  Consensus   ********** ********** ********** ****--**** **********

                              151                                              200
      msa137119.2{303_COH1}   AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
      msa137119.2{303_M732}   AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
      msa137119.2{303_m781}   AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
       msa137119.2{303_090}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
    msa137119.2{303_18RS21}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
      msa137119.2{303_2603}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
      msa137119.2{303_A909}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
    msa137119.2{303_CJB110}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
      msa137119.2{303_H36B}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
 msa137119.2{303_JM9130013}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
    msa137119.2{303_1169NT}   AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
                  Consensus   **-******* ********** ********** ********** **********

                              201                                              250
      msa137119.2{303_COH1}   TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
      msa137119.2{303_M732}   TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
      msa137119.2{303_m781}   TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
       msa137119.2{303_090}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
    msa137119.2{303_18RS21}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
      msa137119.2{303_2603}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
```

Table 66: Comparative Sequences relating to SAG 0754

```
      msa137119.2{303_A909}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
    msa137119.2{303_CJB110}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
      msa137119.2{303_H36B}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
 msa137119.2{303_JM9130013}   TAgGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
    msa137119.2{303_1169NT}   TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
                  Consensus   **-******* ********** ********** ********** -*-****-**

                              251                                               300
      msa137119.2{303_COH1}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
      msa137119.2{303_M732}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
      msa137119.2{303_m781}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
       msa137119.2{303_090}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
    msa137119.2{303_18RS21}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
      msa137119.2{303_2603}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
      msa137119.2{303_A909}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
    msa137119.2{303_CJB110}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
      msa137119.2{303_H36B}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
 msa137119.2{303_JM9130013}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
    msa137119.2{303_1169NT}   TTGATATATT AATTGACTGT ATTGGAGCGA TTAAGCCCAA TCAACTAGAT
                  Consensus   ********** ********** ********** ********** **********

                              301                                               350
      msa137119.2{303_COH1}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
      msa137119.2{303_M732}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
      msa137119.2{303_m781}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
       msa137119.2{303_090}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
    msa137119.2{303_18RS21}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
      msa137119.2{303_2603}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
      msa137119.2{303_A909}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
    msa137119.2{303_CJB110}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
      msa137119.2{303_H36B}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
 msa137119.2{303_JM9130013}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
    msa137119.2{303_1169NT}   GAGCTTAACG TTAAAGCAAC CCAAAAAGCA GTAGCACTCT GTCACAAAAA
                  Consensus   ********** ********** ********** ********** **********

                              351                                               400
      msa137119.2{303_COH1}   TCAAATACCA AAGTTAGTTT AcATTTCAGC CAAtAGCGGC TATTCAGCTT
      msa137119.2{303_M732}   TCAAATACCA AAGTTAGTTT AcATTTCAGC CAAtAGCGGC TATTCAGCTT
      msa137119.2{303_m781}   TCAAATACCA AAGTTAGTTT AcATTTCAGC CAAtAGCGGC TATTCAGCTT
       msa137119.2{303_090}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
    msa137119.2{303_18RS21}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
      msa137119.2{303_2603}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
      msa137119.2{303_A909}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
    msa137119.2{303_CJB110}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
      msa137119.2{303_H36B}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
 msa137119.2{303_JM9130013}   TCAAATACCA AAGTTAGTTT AtATTTCAGC CAAcAGCGGC TATTCAGCTT
    msa137119.2{303_1169NT}   TCAAATACCA AAGTTAGTTT AcATTTCAGC CAAcAGCGGC TATTCAGCTT
                  Consensus   ********** ********** *-******** ***-****** **********

                              401                                               450
      msa137119.2{303_COH1}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
      msa137119.2{303_M732}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
      msa137119.2{303_m781}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
       msa137119.2{303_090}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
    msa137119.2{303_18RS21}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
      msa137119.2{303_2603}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
      msa137119.2{303_A909}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
    msa137119.2{303_CJB110}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
      msa137119.2{303_H36B}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
 msa137119.2{303_JM9130013}   ACATTAaAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
    msa137119.2{303_1169NT}   ACATTAgAAG TAAAAGGAAG GCAGAGCAGA TAATCAAAGC AAGCGGTCTG
                  Consensus   ******-*** ********** ********** ********** **********

                              451                                               500
      msa137119.2{303_COH1}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
      msa137119.2{303_M732}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
      msa137119.2{303_m781}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
       msa137119.2{303_090}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
    msa137119.2{303_18RS21}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
      msa137119.2{303_2603}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
      msa137119.2{303_A909}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
    msa137119.2{303_CJB110}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
      msa137119.2{303_H36B}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
 msa137119.2{303_JM9130013}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
    msa137119.2{303_1169NT}   GATTATCTTT TTGTAAGACC AGGTTTGATG TATGGTGAAG AGCGACCTCT
                  Consensus   ********** ********** ********** ********** **********

                              501                                               550
      msa137119.2{303_COH1}   CTCGATTTTC CAAGCCAAGT GTATAAAaTT ATTTAGTCAT TTGCCTTTCT
      msa137119.2{303_M732}   CTCGATTTTC CAAGCCAAGT GTATAAAaTT ATTTAGTCAT TTGCCTTTCT
      msa137119.2{303_m781}   CTCGATTTTC CAAGCCAAGT GTATAAAaTT ATTTAGTCAT TTGCCTTTCT
       msa137119.2{303_090}   CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
    msa137119.2{303_18RS21}   CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
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Table 66: Comparative Sequences relating to SAG 0754

```
     msa137119.2{303_2603}  CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
     msa137119.2{303_A909}  CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
   msa137119.2{303_CJB110}  CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
     msa137119.2{303_H36B}  CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
msa137119.2{303_JM9130013}  CTCGATTTTC CAAGCCAAGT GTATAAAgTT ATTTAGTCAT TTGCCTTTCT
   msa137119.2{303_1169NT}  CTCGATTTTC CAAGCCAAGT GTATAAAaTT ATTTAGTCAT TTGCCTTTCT
                 Consensus  ********** ********** *******-** ********** **********

                            551                                                600
     msa137119.2{303_COH1}  TAGGTATTGT TGTACAAAAa GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
     msa137119.2{303_M732}  TAGGTATTGT TGTACAAAAa GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
     msa137119.2{303_m781}  TAGGTATTGT TGTACAAAAa GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
      msa137119.2{303_090}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
   msa137119.2{303_18RS21}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
     msa137119.2{303_2603}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
     msa137119.2{303_A909}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
   msa137119.2{303_CJB110}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
     msa137119.2{303_H36B}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
msa137119.2{303_JM9130013}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
   msa137119.2{303_1169NT}  TAGGTATTGT TGTACAAAAg GTCTTTCCAA CTAAGGTTGT GATAGTGGCA
                 Consensus  ********** *********- ********** ********** **********

                            601                                                650
     msa137119.2{303_COH1}  GAAGCAATCG TTACTtCGCT TAGGAaAAAA CCAACtCAAA AAATCCTTTC
     msa137119.2{303_M732}  GAAGCAATCG TTACTtCGCT TAGGAaAAAA CCAACtCAAA AAATCCTTTC
     msa137119.2{303_m781}  GAAGCAATCG TTACTtCGCT TAGGAaAAAA CCAACtCAAA AAATCCTTTC
      msa137119.2{303_090}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
   msa137119.2{303_18RS21}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
     msa137119.2{303_2603}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
     msa137119.2{303_A909}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
   msa137119.2{303_CJB110}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
     msa137119.2{303_H36B}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
msa137119.2{303_JM9130013}  GAAGCAATCG TTACTaCGCT TAGGAaAAAA CCAACcCAAA AAATCCTTTC
   msa137119.2{303_1169NT}  GAAGCAATCG TTACTaCGCT TAGGAcAAAA CCAACtCAAA AAATCCTTTC
                 Consensus  ********** *****-**** *****-**** *****-**** **********

                            651                  672
     msa137119.2{303_COH1}  TATTGAAGAA TTAAATAATA AA
     msa137119.2{303_M732}  TATTGAAGAA TTAAATAATA AA
     msa137119.2{303_m781}  TATTGAAGAA TTAAATAATA AA
      msa137119.2{303_090}  TATTGAAGAA TTAAATAATA AA
   msa137119.2{303_18RS21}  TATTGAAGAA TTAAATAATA AA
     msa137119.2{303_2603}  TATTGAAGAA TTAAATAATA AA
     msa137119.2{303_A909}  TATTGAAGAA TTAAATAATA AA
   msa137119.2{303_CJB110}  TATTGAAGAA TTAAATAATA AA
     msa137119.2{303_H36B}  TATTGAAGAA TTAAATAATA AA
msa137119.2{303_JM9130013}  TATTGAAGAA TTAAATAATA AA
   msa137119.2{303_1169NT}  TATTGAAGAA TTAAATAATA AA
                 Consensus  ********** ********** **
```

SEQ ID NO. 6612

STRAIN 2603 frame: 1

```
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK
```

SEQ ID NO. 6613

STRAIN 090 frame: 1

```
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK
```

SEQ ID NO. 6614

STRAIN A909 frame: 1

```
TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK
```

SEQ ID NO. 6615

STRAIN H36B frame: 2

```
IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL
TYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVY
ISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFL
GIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK
```

SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLTYIKGDIT
EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVYISANSGYS
AYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFLGIVVQKVF
PTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIFKD
PRLTYIKGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIRSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRTKPTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPTKVVIVAEAIVTTLRKKPTQKILSIEELNNK

```
PRETTY of: /biotmp/msa137299.2{*}   April 10, 2003 03:37  ..

                                  1                                                   50
      msa137299.2{303_COH1}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
      msa137299.2{303_M732}  ~~~~~~~~~~ ~QNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
      msa137299.2{303_M781}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
       msa137299.2{303_090}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
    msa137299.2{303_18RS21}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
      msa137299.2{303_2603}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
      msa137299.2{303_A909}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
    msa137299.2{303_CJB110}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
 msa137299.2{303_JM9130013}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
      msa137299.2{303_H36B}  ~~~ikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKvAYLSR
    msa137299.2{303_1169NT}  trhikisiln lQNEGEGTME ILIAGGSGFL GKQIIKAALT KGHKlAYLSR
                  Consensus  ---------- -********* ********** ********** ****-*****

                             51                                                  100
      msa137299.2{303_COH1}  HEGKGDIFKD PRLTYIkGDI TEADKIHLEh RnFDILIDCI GAIKPNQLDE
      msa137299.2{303_M732}  HEGKGDIFKD PRLTYIkGDI TEADKIHLEh RnFDILIDCI GAIKPNQLDE
      msa137299.2{303_M781}  HEGKGDIFKD PRLTYIkGDI TEADKIHLEh RnFDILIDCI GAIKPNQLDE
       msa137299.2{303_090}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
    msa137299.2{303_18RS21}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
      msa137299.2{303_2603}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
      msa137299.2{303_A909}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
    msa137299.2{303_CJB110}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
 msa137299.2{303_JM9130013}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
      msa137299.2{303_H36B}  HEGKGDIFKD PRLTYIrGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
    msa137299.2{303_1169NT}  HEGKGDIFKD PRLTYIkGDI TEADKIHLEd RtFDILIDCI GAIKPNQLDE
                  Consensus  ********** ******-*** *********- *-******** **********
```

Table 66: Comparative Sequences relating to SAG 0754

```
                              101                                                150
     msa137299.2{303_COH1}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
     msa137299.2{303_M732}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
     msa137299.2{303_M781}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
      msa137299.2{303_090}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
   msa137299.2{303_18RS21}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
     msa137299.2{303_2603}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
     msa137299.2{303_A909}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
   msa137299.2{303_CJB110}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
msa137299.2{303_JM9130013}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
     msa137299.2{303_H36B}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIkSKRKA EQIIKASGLD
   msa137299.2{303_1169NT}    LNVKATQKAV ALCHKNQIPK LVYISANSGY SAYIrSKRKA EQIIKASGLD
                 Consensus    ********** ********** ********** ****-***** **********

                              151                                                200
     msa137299.2{303_COH1}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
     msa137299.2{303_M732}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
     msa137299.2{303_M781}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
      msa137299.2{303_090}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
   msa137299.2{303_18RS21}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
     msa137299.2{303_2603}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
     msa137299.2{303_A909}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
   msa137299.2{303_CJB110}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_JM9130013}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
     msa137299.2{303_H36B}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
   msa137299.2{303_1169NT}    YLFVRPGLMY GEERPLSIFQ AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
                 Consensus    ********** ********** ********** ********** **********

                              201                  223
     msa137299.2{303_COH1}    AIVTsLRkKP TQKILSIEEL NNK
     msa137299.2{303_M732}    AIVTsLRkKP TQKILSIEEL NNK
     msa137299.2{303_M781}    AIVTsLRkKP TQKILSIEEL NNK
      msa137299.2{303_090}    AIVTtLRkKP TQKILSIEEL NNK
   msa137299.2{303_18RS21}    AIVTtLRkKP TQKILSIEEL NNK
     msa137299.2{303_2603}    AIVTtLRkKP TQKILSIEEL NNK
     msa137299.2{303_A909}    AIVTtLRkKP TQKILSIEEL NNK
   msa137299.2{303_CJB110}    AIVTtLRkKP TQKILSIEEL NNK
msa137299.2{303_JM9130013}    AIVTtLRkKP TQKILSIEEL NNK
     msa137299.2{303_H36B}    AIVTtLRkKP TQKILSIEEL NNK
   msa137299.2{303_1169NT}    AIVTtLRtKP TQKILSIEEL NNK
                 Consensus    ****-**-** ********** ***
```

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701
STRAIN 090
CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCCGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTG
AAGTTGTTCAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA
AGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
ATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGcTAAAACTAC
TAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTTAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGT
CCGTGGTGATGAATTCATTGATACtTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702
STRAIN A909
CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCTGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTG
AAGTTGTTCAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA
AGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATT
ATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTAC
TAAAGCaACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAnAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAgAGAAA
CTTTAAGCAATTTTGGAGGtGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGT
CCGTGGTGATGAATTCATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703
STRAIN H36B
GGACGAGTAATGAAAACAATAACAACATTTGAAAAT
AAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG
TTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
TTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTG
GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACAT
GATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCAT
TAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTTAGTT
TCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAAC
GACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTTGT
TAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTGCGAAT
GATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGT
TAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCCAACTC
ATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAAT
ATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTAATCA
AGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCCTT
TCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT
TTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTCCCAGG
AAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG
CTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGGAGGT
GTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTAGTTTCTA
TAACGACAGCAAG

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704
STRAIN 18RS21
GGACGAGTAATGAAAACAATAACAACATTTG
AAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCT
GCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
ACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTA
AAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGT
TACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
AGCATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACT
TAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACG
ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGG
TTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTG
CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATG
GGAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCC
AACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAT
GGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTT
AATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGT
TCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGC
AACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTC
CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA
ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTG
GAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTAGT
TTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATT
ATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATC
GCGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACAT
ATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
AGCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATA
AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCA
AATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATT
CATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705
STRAIN M732
GGACGAGTAATGAAAACAATAACAACATTTGAAA
ATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA
CGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC
ATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAG
TGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTAC
ATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC
ATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTTAG
TTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACA
ACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTT
GTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTGCGG
aTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGA
GTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCCAAC
TCAtTTAGATTATCATGGGTCTTTTGAAGATTATGtTGCTGCAAAATGGA
ATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTAAT
CAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAaTCGTTCC
TTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAAC
TTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTCCCA
GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT
AGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGGAG
GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTAGTTTC
TATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTATC
TGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCGCG
GTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATATG
GTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAAGC
AGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG
CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAAAT
GCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATTCAT
TGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706
STRAIN COH1
GGACGAGTAATGAAAACAATAACAACATTTGA
AAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
CACGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA
CCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTT
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAA
GCATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTT
AGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGA
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGT
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTGC
GGaTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG
GAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCCA
ACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATG
GAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTA
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAaCAATCGTT
CCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA
ACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTCC
CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTAGTT
TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA
TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAA
ATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATTC
ATTGATACTTTCGAAA

SEQ ID NO. 6707
STRAIN M781
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TGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCG
CTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC
AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT
TAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTT
GTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA
AAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATA
CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAA
CGACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGA
GGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGC
TGCGGATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAA
TGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATG
CCAACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAA
ATGGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATT
TTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAaCAATC
GTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAA
GCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTG
TCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCT
AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTT
TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTA
GTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCA
TTATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGA
TCGCGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAAC
ATATGGTTGTTTTAgGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAA
AAAGCAGGAGTaACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA
TAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTG
CAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAA
TTCATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708
STRAIN CJB110
GGACGAGTAATGAAAACAATAACAACATTTGA
AAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
CACGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA
CCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTT
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAA
GCATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTT
AGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGA
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGT
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAGGCTGC
GGATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG
GAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAATGCCA
ACTCATTTAGATTATCATGGGTCTTTTGAAGAATATGTTGCTGCAAAATG
GAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTA
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTT
CCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA
ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTCC
CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA
CTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTATTAGTT
TCTATAATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA
TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAA
ATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATTC
ATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709
STRAIN 1169NT
CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA
TCTGGAGAAGCCGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTGAATGC

Table 67: Comparative Sequences relating to SAG0475

TGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTG
AAGTTGTTCAGGCTGCGGATGATAAAGATACTCTAGTTATGGAATTATCA
AGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGAtT
ATGtTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGcTAAAACTAC
TAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
GACGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTCATGGTATTAGTTTCTATAACGACAGTAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAGCATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCAATGCTTTAgATGTTA
GAgATGCgGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGTTmAGTcCTGCGAATGCATCATGGGACATGTATAAGAATTTCGAAGT
CCGTGGTGATGAATTCATTGATACTTTCG

SEQ ID NO. 6710
STRAIN JM9130013
GGACGAGTAATGAAAACAATAACAACA
TTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGC
TGCTGCACGTTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG
GCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGT
ATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGtTAGATGAGGATTT
TTGTTACATGATTaAAAATCCAGGAATACCTTATAACAATCCTATGGTCA
AAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCA
TACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA
AACGACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGA
GAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAG
GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCT
AATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAATTTAA
TGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCA
AAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAA
TTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCaACAA
TCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGAC
AAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGG
TGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTG
CTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAAT
TTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTCATGGTAT
TAGtTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAG
CATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTT
GATCGCAGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAA
ACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCAC
AAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTA
CATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCC
TGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATG
AATTCATTGATACtTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710
STRAIN 2603
ggacgagtaatgaaaacaataacaacatttgaaaataaaaaagttttagt
ccttggtttagcacgatctggagaagctgctgcacgtttgttagctaagt
taggagcaatagtgacagttaatgatggcaaaccatttgatgaaaatcca
acagcacagtctttgttggaagagggtattaaagtggtttgtggtagtca
tcctttagaattgttagatgaggattttgttacatgattaaaaatccag
gaataccttataacaatcctatggtcaaaaaagcattagaaaaacaaatc
cctgttttgactgaagtggaattagcatacttagtttcagaatctcagct
aataggtattacaggctctaacgggaaaacgacaacgacaacgatgattg
cagaagtcttaaatgctggaggtcagagaggtttgttagctgggaatatc
ggctttcctgctagtgaagttgttcaggctgcgaatgataaagatactct
agttatggaattatcaagttttcagctaatgggagttaaggaatttcgtc
ctcatattgcagtaattactaatttaatgccaactcatttagattatcat
gggtcttttgaagattatgttgctgcaaaatggaatatccaaaatcaaat
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agttagctaaaactactaaagcaacaatcgttcctttctctactacggaa
aaagttgatggtgcttacgtacaagacaagcaacttttctataaagggga
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agaatgctctagcaactattgcggttgctaaactggctggtatcagtaat
caagttattagagaaactttaagcaattttggaggtgttaaacaccgctt
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caactaatatattggcaactcaaaaagcattatctggctttgataatact
aaagttatcctaattgcaggaggtcttgatcgcggtaatgagtttgatga
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cggcatctcgagtaaaacgtgctgcacaaaaagcaggagtaacttatagc
gatgctttagatgttagagatgcggtacataaagcttatgaggtggcaca
acagggcgatgttatcttgctaagtcctgcaaatgcatcatgggacatgt
ataagaatttcgaagtccgtggtgatgaattcattgatactttcgaaagt
cttagaggagag

Table 67: Comparative Sequences relating to SAG0475

```
MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa30176.2{*}   April 29, 2002 02:09  ..

                                   1                                                  50
     msa30176.2{305_18RS21}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
       msa30176.2{305_2603}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
       msa30176.2{305_A909}   ~~~~~~~~~~ ~~~~~~CAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
       msa30176.2{305_H36B}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
  msa30176.2{305_JM9130013}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
       msa30176.2{305_COH1}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
       msa30176.2{305_M781}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
      msa30176.2{305e_M732}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
        msa30176.2{305_090}   ~~~~~~~~~~ ~~~~~~CAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
     msa30176.2{305_CJB110}   ggacgagtaa tgaaaaCAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
    msa30176.2{305_1169NT}    ~~~~~~~~~~ ~~~~~~CAAT AACAACATTT GAAAATAAAA AAGTTTTAGT
                  Consensus   ---------- ------**** ********** ********** **********

                              51                                                 100
     msa30176.2{305_18RS21}   CCTTGGTTTA GCACGATCTG GAGAAGCtGC TGCACGTTTG TTAGCTAAGT
       msa30176.2{305_2603}   CCTTGGTTTA GCACGATCTG GAGAAGCtGC TGCACGTTTG TTAGCTAAGT
       msa30176.2{305_A909}   CCTTGGTTTA GCACGATCTG GAGAAGCtGC TGCACGTTTG TTAGCTAAGT
       msa30176.2{305_H36B}   CCTTGGTTTA GCACGATCTG GAGAAGCtGC TGCACGTTTG TTAGCTAAGT
  msa30176.2{305_JM9130013}   CCTTGGTTTA GCACGATCTG GAGAAGCtGC TGCACGTTTG TTAGCTAAGT
       msa30176.2{305_COH1}   CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
       msa30176.2{305_M781}   CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
      msa30176.2{305e_M732}   CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
        msa30176.2{305_090}   CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
     msa30176.2{305_CJB110}   CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
    msa30176.2{305_1169NT}    CCTTGGTTTA GCACGATCTG GAGAAGCcGC TGCACGTTTG TTAGCTAAGT
                  Consensus   ********** ********** *******_** ********** **********

                              101                                                150
     msa30176.2{305_18RS21}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
       msa30176.2{305_2603}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
       msa30176.2{305_A909}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
       msa30176.2{305_H36B}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
  msa30176.2{305_JM9130013}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
       msa30176.2{305_COH1}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
       msa30176.2{305_M781}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
      msa30176.2{305e_M732}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
        msa30176.2{305_090}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
     msa30176.2{305_CJB110}   TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
    msa30176.2{305_1169NT}    TAGGAGCAAT AGTGACAGTT AATGATGGCA AACCATTTGA TGAAAATCCA
                  Consensus   ********** ********** ********** ********** **********

                              151                                                200
     msa30176.2{305_18RS21}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
       msa30176.2{305_2603}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
       msa30176.2{305_A909}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
       msa30176.2{305_H36B}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
  msa30176.2{305_JM9130013}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
       msa30176.2{305_COH1}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
       msa30176.2{305_M781}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
      msa30176.2{305e_M732}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
        msa30176.2{305_090}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
     msa30176.2{305_CJB110}   ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
    msa30176.2{305_1169NT}    ACAGCACAGT CTTTGTTGGA AGAGGGTATT AAAGTGGTTT GTGGTAGTCA
                  Consensus   ********** ********** ********** ********** **********

                              201                                                250
     msa30176.2{305_18RS21}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
       msa30176.2{305_2603}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
       msa30176.2{305_A909}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
       msa30176.2{305_H36B}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
  msa30176.2{305_JM9130013}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
       msa30176.2{305_COH1}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
       msa30176.2{305_M781}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
      msa30176.2{305e_M732}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
        msa30176.2{305_090}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
     msa30176.2{305_CJB110}   TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
    msa30176.2{305_1169NT}    TCCTTTAGAA TTGTTAGATG AGGATTTTTG TTACATGATT AAAAATCCAG
                  Consensus   ********** ********** ********** ********** **********

                              251                                                300
     msa30176.2{305_18RS21}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
       msa30176.2{305_2603}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
       msa30176.2{305_A909}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
       msa30176.2{305_H36B}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
  msa30176.2{305_JM9130013}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
       msa30176.2{305_COH1}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
       msa30176.2{305_M781}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
      msa30176.2{305e_M732}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
        msa30176.2{305_090}   GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
```

Table 67: Comparative Sequences relating to SAG0475

```
   msa30176.2{305_CJB110}  GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
  msa30176.2{305_1169NT}  GAATACCTTA TAACAATCCT ATGGTCAAAA AAGCATTAGA AAAACAAATC
               Consensus  ********** ********** ********** ********** **********

                          301                                                350
   msa30176.2{305_18RS21}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
     msa30176.2{305_2603}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
     msa30176.2{305_A909}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
     msa30176.2{305_H36B}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
msa30176.2{305_JM9130013}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
     msa30176.2{305_COH1}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
     msa30176.2{305_M781}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
    msa30176.2{305e_M732}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
      msa30176.2{305_090}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
   msa30176.2{305_CJB110}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
   msa30176.2{305_1169NT}  CCTGTTTTGA CTGAAGTGGA ATTAGCATAC TTAGTTTCAG AATCTCAGCT
                Consensus  ********** ********** ********** ********** **********

                          351                                                400
   msa30176.2{305_18RS21}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
     msa30176.2{305_2603}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
     msa30176.2{305_A909}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
     msa30176.2{305_H36B}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
msa30176.2{305_JM9130013}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
     msa30176.2{305_COH1}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
     msa30176.2{305_M781}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
    msa30176.2{305e_M732}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
      msa30176.2{305_090}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
   msa30176.2{305_CJB110}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
   msa30176.2{305_1169NT}  AATAGGTATT ACAGGCTCTA ACGGGAAAAC GACAACGACA ACGATGATTG
                Consensus  ********** ********** ********** ********** **********

                          401                                                450
   msa30176.2{305_18RS21}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
     msa30176.2{305_2603}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
     msa30176.2{305_A909}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
     msa30176.2{305_H36B}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
msa30176.2{305_JM9130013}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
     msa30176.2{305_COH1}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
     msa30176.2{305_M781}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
    msa30176.2{305e_M732}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
      msa30176.2{305_090}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
   msa30176.2{305_CJB110}  CAGAAGTCTT aAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
   msa30176.2{305_1169NT}  CAGAAGTCTT gAATGCTGGA GGTCAGAGAG GTTTGTTAGC TGGGAATATC
                Consensus  ********** -********* ********** ********** **********

                          451                                                500
   msa30176.2{305_18RS21}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGaATGATA AAGATAcTCT
     msa30176.2{305_2603}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGaATGATA AAGATAcTCT
     msa30176.2{305_A909}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGaATGATA AAGATAcTCT
     msa30176.2{305_H36B}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGaATGATA AAGATAcTCT
msa30176.2{305_JM9130013}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGaATGATA AAGATAcTCT
     msa30176.2{305_COH1}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAtTCT
     msa30176.2{305_M781}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAtTCT
    msa30176.2{305e_M732}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAtTCT
      msa30176.2{305_090}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAtTCT
   msa30176.2{305_CJB110}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAtTCT
   msa30176.2{305_1169NT}  GGCTTTCCTG CTAGTGAAGT TGTTCAGGCT GCGgATGATA AAGATAcTCT
                Consensus  ********** ********** ********** ***-****** ******-***

                          501                                                550
   msa30176.2{305_18RS21}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
     msa30176.2{305_2603}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
     msa30176.2{305_A909}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
     msa30176.2{305_H36B}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
msa30176.2{305_JM9130013}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
     msa30176.2{305_COH1}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
     msa30176.2{305_M781}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
    msa30176.2{305e_M732}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
      msa30176.2{305_090}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
   msa30176.2{305_CJB110}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
   msa30176.2{305_1169NT}  AGTTATGGAA TTATCAAGTT TTCAGCTAAT GGGAGTTAAG GAATTTCGTC
                Consensus  ********** ********** ********** ********** **********

                          551                                                600
   msa30176.2{305_18RS21}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
     msa30176.2{305_2603}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
     msa30176.2{305_A909}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
     msa30176.2{305_H36B}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
msa30176.2{305_JM9130013}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
     msa30176.2{305_COH1}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
     msa30176.2{305_M781}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
    msa30176.2{305e_M732}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
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Table 67: Comparative Sequences relating to SAG0475

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      msa30176.2{305_090}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
   msa30176.2{305_CJB110}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
   msa30176.2{305_1169NT}  CTCATATTGC AGTAATTACT AATTTAATGC CAACTCATTT AGATTATCAT
                Consensus  ********** ********** ********** ********** **********

                           601                                                650
   msa30176.2{305_18RS21}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
     msa30176.2{305_2603}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
     msa30176.2{305_A909}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
     msa30176.2{305_H36B}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
msa30176.2{305_JM9130013}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
     msa30176.2{305_COH1}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
     msa30176.2{305_M781}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
    msa30176.2{305e_M732}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
      msa30176.2{305_090}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
   msa30176.2{305_CJB110}  GGGTCTTTTG AAGAaTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
   msa30176.2{305_1169NT}  GGGTCTTTTG AAGAtTATGT TGCTGCAAAA TGGAATATCC AAAATCAAAT
                Consensus  ********** ****_***** ********** ********** **********

                           651                                                700
   msa30176.2{305_18RS21}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
     msa30176.2{305_2603}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
     msa30176.2{305_A909}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
     msa30176.2{305_H36B}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
msa30176.2{305_JM9130013}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
     msa30176.2{305_COH1}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
     msa30176.2{305_M781}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
    msa30176.2{305e_M732}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
      msa30176.2{305_090}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
   msa30176.2{305_CJB110}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
   msa30176.2{305_1169NT}  GTCTTCATCT GATTTTTTGG TACTTAATTT TAATCAAGGT ATTTCTAAAG
                Consensus  ********** ********** ********** ********** **********

                           701                                                750
   msa30176.2{305_18RS21}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
     msa30176.2{305_2603}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
     msa30176.2{305_A909}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
     msa30176.2{305_H36B}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
msa30176.2{305_JM9130013}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
     msa30176.2{305_COH1}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
     msa30176.2{305_M781}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
    msa30176.2{305e_M732}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
      msa30176.2{305_090}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
   msa30176.2{305_CJB110}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
   msa30176.2{305_1169NT}  AGTTAGCTAA AACTACTAAA GCAACAATCG TTCCTTTCTC TACTACGGAA
                Consensus  ********** ********** ********** ********** **********

                           751                                                800
   msa30176.2{305_18RS21}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
     msa30176.2{305_2603}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
     msa30176.2{305_A909}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
     msa30176.2{305_H36B}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
msa30176.2{305_JM9130013}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
     msa30176.2{305_COH1}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
     msa30176.2{305_M781}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
    msa30176.2{305e_M732}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
      msa30176.2{305_090}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
   msa30176.2{305_CJB110}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
   msa30176.2{305_1169NT}  AAAGTTGATG GTGCTTACGT ACAAGACAAG CAACTTTTCT ATAAAGGGGA
                Consensus  ********** ********** ********** ********** **********

                           801                                                850
   msa30176.2{305_18RS21}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
     msa30176.2{305_2603}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
     msa30176.2{305_A909}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAn
     msa30176.2{305_H36B}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
msa30176.2{305_JM9130013}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
     msa30176.2{305_COH1}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
     msa30176.2{305_M781}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
    msa30176.2{305e_M732}  GAATATTATG TcAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
      msa30176.2{305_090}  GAATATTATG TtAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
   msa30176.2{305_CJB110}  GAATATTATG TtAGTAGAtG ACATTGGTGT CCCAGGAAGC CATAACGTAg
   msa30176.2{305_1169NT}  GAATATTATG TcAGTAGAcG ACATTGGTGT CCCAGGAAGC CATAACGTAg
                Consensus  ********** *_******_* ********** ********** *********_

                           851                                                900
   msa30176.2{305_18RS21}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTgGCTGG TATCAGTAAT
     msa30176.2{305_2603}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTgGCTGG TATCAGTAAT
     msa30176.2{305_A909}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTgGCTGG TATCAGTAAT
     msa30176.2{305_H36B}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTgGCTGG TATCAGTAAT
msa30176.2{305_JM9130013}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTgGCTGG TATCAGTAAT
     msa30176.2{305_COH1}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
     msa30176.2{305_M781}  AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
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Table 67: Comparative Sequences relating to SAG0475

```
      msa30176.2{305e_M732}   AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
       msa30176.2{305_090}    AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
     msa30176.2{305_CJB110}   AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
     msa30176.2{305_1169NT}   AGAATGCTCT AGCAACTATT GCGGTTGCTA AACTaGCTGG TATCAGTAAT
                  Consensus   ********** ********** ********** ****_***** **********

                              901                                               950
     msa30176.2{305_18RS21}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
       msa30176.2{305_2603}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
       msa30176.2{305_A909}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
       msa30176.2{305_H36B}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
  msa30176.2{305_JM9130013}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
       msa30176.2{305_COH1}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
       msa30176.2{305_M781}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
      msa30176.2{305e_M732}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
        msa30176.2{305_090}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
     msa30176.2{305_CJB110}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
     msa30176.2{305_1169NT}   CAAGTTATTA GAGAAACTTT AAGCAATTTT GGAGGTGTTA AACACCGCTT
                  Consensus   ********** ********** ********** ********** **********

                              951                                              1000
     msa30176.2{305_18RS21}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
       msa30176.2{305_2603}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
       msa30176.2{305_A909}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
       msa30176.2{305_H36B}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAG~
  msa30176.2{305_JM9130013}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
       msa30176.2{305_COH1}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
       msa30176.2{305_M781}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
      msa30176.2{305e_M732}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
        msa30176.2{305_090}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGcAAGt
     msa30176.2{305_CJB110}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAt GACAGcAAGt
     msa30176.2{305_1169NT}   GCAATCACTC GGTAAGGTTC ATGGTATTAG TTTCTATAAc GACAGtAAGt
                  Consensus   ********** ********** ********** *********_ *****_***_

                              1001                                             1050
     msa30176.2{305_18RS21}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
       msa30176.2{305_2603}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
       msa30176.2{305_A909}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
       msa30176.2{305_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa30176.2{305_JM9130013}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
       msa30176.2{305_COH1}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
       msa30176.2{305_M781}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
      msa30176.2{305e_M732}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
        msa30176.2{305_090}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
     msa30176.2{305_CJB110}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
     msa30176.2{305_1169NT}   caactaatat attggcaact caaaaagcat tatctggctt tgataatact
                  Consensus   ---------- ---------- ---------- ---------- ----------

                              1051                                             1100
     msa30176.2{305_18RS21}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
       msa30176.2{305_2603}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
       msa30176.2{305_A909}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
       msa30176.2{305_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa30176.2{305_JM9130013}   aaagttatcc taattgcagg aggtcttgat cgcagtaatg agtttgatga
       msa30176.2{305_COH1}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
       msa30176.2{305_M781}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
      msa30176.2{305e_M732}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
        msa30176.2{305_090}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
     msa30176.2{305_CJB110}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
     msa30176.2{305_1169NT}   aaagttatcc taattgcagg aggtcttgat cgcggtaatg agtttgatga
                  Consensus   ---------- ---------- ---------- ---------- ----------

                              1101                                             1150
     msa30176.2{305_18RS21}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
       msa30176.2{305_2603}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
       msa30176.2{305_A909}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
       msa30176.2{305_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa30176.2{305_JM9130013}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
       msa30176.2{305_COH1}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
       msa30176.2{305_M781}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
      msa30176.2{305e_M732}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
        msa30176.2{305_090}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
     msa30176.2{305_CJB110}   attgatacca gatatcactg gacttaaaca tatggttgtt ttaggggaat
     msa30176.2{305_1169NT}   attgatacca gatatcactg gacttaagca tatggttgtt ttaggggaat
                  Consensus   ---------- ---------- ---------- ---------- ----------

                              1151                                             1200
     msa30176.2{305_18RS21}   cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
       msa30176.2{305_2603}   cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
       msa30176.2{305_A909}   cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
       msa30176.2{305_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa30176.2{305_JM9130013}   cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
       msa30176.2{305_COH1}   cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
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Table 67: Comparative Sequences relating to SAG0475

```
     msa30176.2{305_M781}  cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
    msa30176.2{305e_M732}  cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
      msa30176.2{305_090}  cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
   msa30176.2{305_CJB110}  cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
   msa30176.2{305_1169NT}  cggcatctcg agtaaaacgt gctgcacaaa aagcaggagt aacttatagc
                Consensus  ---------- ---------- ---------- ---------- ----------

                           1201                                              1250
   msa30176.2{305_18RS21}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
     msa30176.2{305_2603}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
     msa30176.2{305_A909}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
     msa30176.2{305_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa30176.2{305_JM9130013}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
     msa30176.2{305_COH1}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
     msa30176.2{305_M781}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
    msa30176.2{305e_M732}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
      msa30176.2{305_090}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
   msa30176.2{305_CJB110}  gatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
   msa30176.2{305_1169NT}  aatgctttag atgttagaga tgcggtacat aaagcttatg aggtggcaca
                Consensus  ---------- ---------- ---------- ---------- ----------

                           1251                                              1300
   msa30176.2{305_18RS21}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
     msa30176.2{305_2603}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
     msa30176.2{305_A909}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
     msa30176.2{305_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa30176.2{305_JM9130013}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
     msa30176.2{305_COH1}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
     msa30176.2{305_M781}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
    msa30176.2{305e_M732}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
      msa30176.2{305_090}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
   msa30176.2{305_CJB110}  acagggcgat gttatcttgc taagtcctgc aaatgcatca tgggacatgt
   msa30176.2{305_1169NT}  acagggcgat gttatcttgt tmagtcctgc gaatgcatca tgggacatgt
                Consensus  ---------- ---------- ---------- ---------- ----------

                           1301                                              1350
   msa30176.2{305_18RS21}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
     msa30176.2{305_2603}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
     msa30176.2{305_A909}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
     msa30176.2{305_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa30176.2{305_JM9130013}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
     msa30176.2{305_COH1}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaa~~
     msa30176.2{305_M781}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
    msa30176.2{305e_M732}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
      msa30176.2{305_090}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
   msa30176.2{305_CJB110}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcgaaagt
   msa30176.2{305_1169NT}  ataagaattt cgaagtccgt ggtgatgaat tcattgatac tttcg~~~~~
                Consensus  ---------- ---------- ---------- ---------- ----------

                           1351     1362
   msa30176.2{305_18RS21}  cttagaggag ag
     msa30176.2{305_2603}  cttagaggag ag
     msa30176.2{305_A909}  cttagaggag ag
     msa30176.2{305_H36B}  ~~~~~~~~~~ ~~
msa30176.2{305_JM9130013}  cttagaggag ag
     msa30176.2{305_COH1}  ~~~~~~~~~~ ~~
     msa30176.2{305_M781}  cttagaggag ag
    msa30176.2{305e_M732}  cttagaggag ag
      msa30176.2{305_090}  cttagaggag ag
   msa30176.2{305_CJB110}  cttagaggag ag
   msa30176.2{305_1169NT}  ~~~~~~~~~~ ~~
                Consensus  ---------- --
```

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
TTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
TTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET
LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSK

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEEYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
TTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGDVILXSP
ANASWDMYKNFEVRGDEFIDTF

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

```
GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE
```

SEQ ID NO. 6721

STRAIN 2603 frame: 1

```
GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGI
TGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE
```

MSA Alignment Results: Pretty output

```
PRETTY of: /biotmp/msa25243.2{*}   April 29, 2002 02:20  ..

                           1                                                  50
   msa25243.2{305_18RS21}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_2603}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_JM9130013}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_COH1}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_M732}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_M781}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
   msa25243.2{305_1169NT}  ~~~~~~ITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_A909}  ~~~~~~ITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
   msa25243.2{305_CJB110}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
      msa25243.2{305_090}  ~~~~~~ITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
     msa25243.2{305_H36B}  grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAIVTV NDGKPFDENP
                Consensus  ------**** ********** ********** ********** **********

                           51                                                100
   msa25243.2{305_18RS21}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_2603}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_JM9130013}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_COH1}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_M732}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_M781}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
   msa25243.2{305_1169NT}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_A909}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
   msa25243.2{305_CJB110}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
      msa25243.2{305_090}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
     msa25243.2{305_H36B}  TAQSLLEEGI KVVCGSHPLE LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
                Consensus  ********** ********** ********** ********** **********

                           101                                               150
   msa25243.2{305_18RS21}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_2603}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_COH1}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_M732}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_M781}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
   msa25243.2{305_1169NT}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_A909}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
   msa25243.2{305_CJB110}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
      msa25243.2{305_090}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
     msa25243.2{305_H36B}  PVLTEVELAY LVSESQLIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
                Consensus  ********** ********** ********** ********** **********

                           151                                               200
   msa25243.2{305_18RS21}  GFPASEVVQA AnDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_2603}  GFPASEVVQA AnDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013}  GFPASEVVQA AnDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_COH1}  GFPASEVVQA AdDKDiLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_M732}  GFPASEVVQA AdDKDiLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_M781}  GFPASEVVQA AdDKDiLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
   msa25243.2{305_1169NT}  GFPASEVVQA AdDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_A909}  GFPASEVVQA AnDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
   msa25243.2{305_CJB110}  GFPASEVVQA AdDKDiLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
      msa25243.2{305_090}  GFPASEVVQA AdDKDiLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
     msa25243.2{305_H36B}  GFPASEVVQA AnDKDtLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
                Consensus  ********** *-***-**** ********** ********** **********
```

Table 67: Comparative Sequences relating to SAG0475

```
                           201                                                250
   msa25243.2{305_18RS21}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_2603}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
msa25243.2{305_JM9130013}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_COH1}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_M732}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_M781}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
   msa25243.2{305_1169NT}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_A909}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
   msa25243.2{305_CJB110}  GSFEeYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
      msa25243.2{305_090}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
     msa25243.2{305_H36B}  GSFEdYVAAK WNIQNQMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE
                Consensus  ****-***** ********** ********** ********** **********

                           251                                                300
   msa25243.2{305_18RS21}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_2603}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
msa25243.2{305_JM9130013}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_COH1}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_M732}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_M781}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
   msa25243.2{305_1169NT}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_A909}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVxNALATI AVAKLAGISN
   msa25243.2{305_CJB110}  KVDGAYVQDK QLFYKGENIM lVDDIGVPGS HNVeNALATI AVAKLAGISN
      msa25243.2{305_090}  KVDGAYVQDK QLFYKGENIM lVDDIGVPGS HNVeNALATI AVAKLAGISN
     msa25243.2{305_H36B}  KVDGAYVQDK QLFYKGENIM sVDDIGVPGS HNVeNALATI AVAKLAGISN
                Consensus  ********** ********** -********* ***-****** **********

                           301                                                350
   msa25243.2{305_18RS21}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_2603}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
msa25243.2{305_JM9130013}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_COH1}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_M732}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_M781}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
   msa25243.2{305_1169NT}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_A909}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
   msa25243.2{305_CJB110}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
      msa25243.2{305_090}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt
     msa25243.2{305_H36B}  QVIRETLSNF GGVKHRLQSL GKVHGISFYN DSK~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ********** ********** ***------- ----------

                           351                                                400
   msa25243.2{305_18RS21}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_2603}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
msa25243.2{305_JM9130013}  kviliaggld rsnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_COH1}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_M732}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_M781}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
   msa25243.2{305_1169NT}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_A909}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
   msa25243.2{305_CJB110}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
      msa25243.2{305_090}  kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aaqkagvtys
     msa25243.2{305_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ---------- ---------- ---------- ---------- ----------

                           401                                                450
   msa25243.2{305_18RS21}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
     msa25243.2{305_2603}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
msa25243.2{305_JM9130013}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
     msa25243.2{305_COH1}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfe~
     msa25243.2{305_M732}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
     msa25243.2{305_M781}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
   msa25243.2{305_1169NT}  naldvrdavh kayevaqqgd vilxspanas wdmyknfevr gdefidtf~~
     msa25243.2{305_A909}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
   msa25243.2{305_CJB110}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
      msa25243.2{305_090}  daldvrdavh kayevaqqgd villspanas wdmyknfevr gdefidtfes
     msa25243.2{305_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ---------- ---------- ---------- ---------- ----------

                           451
   msa25243.2{305_18RS21}  lrge
     msa25243.2{305_2603}  lrge
msa25243.2{305_JM9130013}  lrge
     msa25243.2{305_COH1}  ~~~~
     msa25243.2{305_M732}  lrge
     msa25243.2{305_M781}  lrge
   msa25243.2{305_1169NT}  ~~~~
     msa25243.2{305_A909}  lrge
   msa25243.2{305_CJB110}  lrge
      msa25243.2{305_090}  lrge
     msa25243.2{305_H36B}  ~~~~
                Consensus  ----
```

Table 68: Comparative Sequences relating to SAG 0499

SEQ ID NO. 6801
STRAIN 2603
ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAG
CAAGCGAAACGTGGTGTTATGGCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTAT
GATAAACCAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTA
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
CTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGG
AAGTTACGTCAGGATCATCGTGTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAA
AAAGAAGATTTCAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGTAAAAATGGTATTGTCAAA
GACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCAATTTCACGAAAGATTATGGA
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTT
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGAT
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6802
STRAIN 090
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
TGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGT
GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6803
STRAIN A909
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6804
STRAIN H36B
GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG
GACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGGCAGGAATG
GTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGTGAAAAGGT
TGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAAATATGTTA
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAG
GAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTGTTCGTTCT
ATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTCAAGGAGGG
ACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCTTAATTTGA
TTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGTAAAAATGG
TATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCA
ATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC
ATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGTTATAGAAA
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6805
STRAIN 18RS21
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6806
STRAIN M732
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6807
STRAIN COH1
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGT
GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6808
STRAIN M781
GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGT
GTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6809
STRAIN CJB110
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810
STRAIN 1169NT
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTGCCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811
STRAIN JM9130013
GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

```
PRETTY of: /biotmp/msa236683.2{*}   May 14, 2003 02:57  ..

                            1                                                  50
      msa236683.2{310_090}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
    msa236683.2{310_18RS21}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_2603}  atgGCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_A909}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
    msa236683.2{310_CJB110}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_H36B}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
 msa236683.2{310_JM9130013}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_COH1}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_M732}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
      msa236683.2{310_M781}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
    msa236683.2{310_1169NT}  ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
                  Consensus  ********** ********** ********** ********** **********

                            51                                                100
      msa236683.2{310_090}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
    msa236683.2{310_18RS21}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
      msa236683.2{310_2603}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
      msa236683.2{310_A909}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
    msa236683.2{310_CJB110}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
      msa236683.2{310_H36B}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
 msa236683.2{310_JM9130013}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
      msa236683.2{310_COH1}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAcTG GTGATTAACG
      msa236683.2{310_M732}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAcTG GTGATTAACG
      msa236683.2{310_M781}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAcTG GTGATTAACG
    msa236683.2{310_1169NT}  TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAcTG GTGATTAACG
                  Consensus  ********** ********** ********** *******_** **********
```

Table 68: Comparative Sequences relating to SAG 0499

```
                             101                                                150
      msa236683.2{310_090}   TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
    msa236683.2{310_18RS21}  TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
     msa236683.2{310_2603}   TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
     msa236683.2{310_A909}   TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
    msa236683.2{310_CJB110}  TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
     msa236683.2{310_H36B}   TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
  msa236683.2{310_JM9130013} TTATCAATGG AGAACGTTAT GATAAACCAG GtGAAAAGGT TGCAGACGAT
     msa236683.2{310_COH1}   TTATCAATGG AGAACGTTAT GATAAACCAG GcGAAAAGGT TGCAGACGAT
     msa236683.2{310_M732}   TTATCAATGG AGAACGTTAT GATAAACCAG GcGAAAAGGT TGCAGACGAT
     msa236683.2{310_M781}   TTATCAATGG AGAACGTTAT GATAAACCAG GcGAAAAGGT TGCAGACGAT
    msa236683.2{310_1169NT}  TTATCAATGG AGAACGTTAT GATAAACCAG GcGAAAAGGT TGCAGACGAT
                 Consensus   ********** ********** ********** *-******** **********

                             151                                                200
      msa236683.2{310_090}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
    msa236683.2{310_18RS21}  ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_2603}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_A909}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
    msa236683.2{310_CJB110}  ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_H36B}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
  msa236683.2{310_JM9130013} ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_COH1}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_M732}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
     msa236683.2{310_M781}   ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
    msa236683.2{310_1169NT}  ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG
                 Consensus   ********** ********** ********** ********** **********

                             201                                                250
      msa236683.2{310_090}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
    msa236683.2{310_18RS21}  ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_2603}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_A909}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
    msa236683.2{310_CJB110}  ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_H36B}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
  msa236683.2{310_JM9130013} ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_COH1}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_M732}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
     msa236683.2{310_M781}   ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
    msa236683.2{310_1169NT}  ATTGAAATTA GAAAAAGCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA
                 Consensus   ********** ********** ********** ********** **********

                             251                                                300
      msa236683.2{310_090}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
    msa236683.2{310_18RS21}  AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_2603}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_A909}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
    msa236683.2{310_CJB110}  AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_H36B}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
  msa236683.2{310_JM9130013} AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_COH1}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_M732}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
     msa236683.2{310_M781}   AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
    msa236683.2{310_1169NT}  AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG
                 Consensus   ********** ********** ********** ********** **********

                             301                                                350
      msa236683.2{310_090}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
    msa236683.2{310_18RS21}  CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_2603}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_A909}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
    msa236683.2{310_CJB110}  CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_H36B}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
  msa236683.2{310_JM9130013} CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_COH1}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_M732}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
     msa236683.2{310_M781}   CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
    msa236683.2{310_1169NT}  CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA
                 Consensus   ********** ********** ********** ********** **********

                             351                                                400
      msa236683.2{310_090}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
    msa236683.2{310_18RS21}  ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_2603}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_A909}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
    msa236683.2{310_CJB110}  ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_H36B}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
  msa236683.2{310_JM9130013} ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_COH1}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_M732}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
     msa236683.2{310_M781}   ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
    msa236683.2{310_1169NT}  ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCGTTCT ATGGAACAAT
                 Consensus   ********** ********** ********** ********** **********
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Table 68: Comparative Sequences relating to SAG 0499

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                           401                                                450
      msa236683.2{310_090} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
   msa236683.2{310_18RS21} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_2603} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_A909} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
   msa236683.2{310_CJB110} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_H36B} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
msa236683.2{310_JM9130013} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_COH1} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_M732} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
     msa236683.2{310_M781} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
   msa236683.2{310_1169NT} ATAATTTTAG GTATGCCCAA AAAGAAGATT TCAAGGAGGG ACTGCCTGAA
                 Consensus ********** ********** ********** ********** **********

                           451                                                500
      msa236683.2{310_090} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
   msa236683.2{310_18RS21} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_2603} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_A909} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
   msa236683.2{310_CJB110} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_H36B} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
msa236683.2{310_JM9130013} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_COH1} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_M732} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
     msa236683.2{310_M781} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTaCCAGC
   msa236683.2{310_1169NT} TTTGCATCGA TAGATGTCTC ATTTATCTCT CTTAATTTGA TTTTgCCAGC
                 Consensus ********** ********** ********** ********** ****_*****

                           501                                                550
      msa236683.2{310_090} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
   msa236683.2{310_18RS21} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_2603} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_A909} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
   msa236683.2{310_CJB110} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_H36B} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
msa236683.2{310_JM9130013} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_COH1} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_M732} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
     msa236683.2{310_M781} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
   msa236683.2{310_1169NT} TCTAAAAGAA ATTTTAGTGG ATGGTGGACA AGTAGTGGCA TTAATTAAAC
                 Consensus ********** ********** ********** ********** **********

                           551                                                600
      msa236683.2{310_090} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
   msa236683.2{310_18RS21} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_2603} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_A909} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
   msa236683.2{310_CJB110} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_H36B} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
msa236683.2{310_JM9130013} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_COH1} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_M732} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
     msa236683.2{310_M781} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
   msa236683.2{310_1169NT} CACAATTTGA AGCAGGTCGT GAGCAAATTG GTAAAAATGG TATTGTCAAA
                 Consensus ********** ********** ********** ********** **********

                           601                                                650
      msa236683.2{310_090} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
   msa236683.2{310_18RS21} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_2603} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_A909} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
   msa236683.2{310_CJB110} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_H36B} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
msa236683.2{310_JM9130013} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_COH1} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_M732} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
     msa236683.2{310_M781} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
   msa236683.2{310_1169NT} GACAAGTTGG TTCATGAAAA GGTTTTGACA ACAGTGACCA ATTTCACGAA
                 Consensus ********** ********** ********** ********** **********

                           651                                                700
      msa236683.2{310_090} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
   msa236683.2{310_18RS21} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
     msa236683.2{310_2603} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
     msa236683.2{310_A909} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
   msa236683.2{310_CJB110} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
     msa236683.2{310_H36B} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
msa236683.2{310_JM9130013} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
     msa236683.2{310_COH1} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC gTTCAAGGTG
     msa236683.2{310_M732} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC gTTCAAGGTG
     msa236683.2{310_M781} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC gTTCAAGGTG
   msa236683.2{310_1169NT} AGATTATGGA TATACGGTTA AACATCTTGA TTTTTCGCCC aTTCAAGGTG
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Table 68: Comparative Sequences relating to SAG 0499

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                  Consensus  ********** ********** ********** ********** _*********

                             701                                                750
       msa236683.2{310_090}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
     msa236683.2{310_18RS21}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_2603}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_A909}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
    msa236683.2{310_CJB110}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_H36B}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
 msa236683.2{310_JM9130013}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_COH1}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_M732}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
      msa236683.2{310_M781}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
    msa236683.2{310_1169NT}  GACATGGAAA TATTGAGTTT TTAATGCATT TGCAAAAGTG TCAAGATCCA
                  Consensus  ********** ********** ********** ********** **********

                             751                                                800
       msa236683.2{310_090}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
    msa236683.2{310_18RS21}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_2603}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_A909}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
    msa236683.2{310_CJB110}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_H36B}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
 msa236683.2{310_JM9130013}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_COH1}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_M732}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
      msa236683.2{310_M781}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
    msa236683.2{310_1169NT}  CAAAATCTTG TGCTTGACCA AATACAAGAT GTTATAGAAA AAGCACATAA
                  Consensus  ********** ********** ********** ********** **********

                             801                    825
       msa236683.2{310_090}  GGAATTTAAG AAAAATGAAG AAGAG
    msa236683.2{310_18RS21}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_2603}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_A909}  GGAATTTAAG AAAAATGAAG AAGAG
    msa236683.2{310_CJB110}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_H36B}  GGAATTTAAG AAAAATGAAG AAGAG
 msa236683.2{310_JM9130013}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_COH1}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_M732}  GGAATTTAAG AAAAATGAAG AAGAG
      msa236683.2{310_M781}  GGAATTTAAG AAAAATGAAG AAGAG
    msa236683.2{310_1169NT}  GGAATTTAAG AAAAATGAAG AAGAG
                  Consensus  ********** ********** *****
```

SEQ ID NO. 6812
STRAIN 2603 frame: 1
MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6813
STRAIN 090 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6814
STRAIN A909 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6815
STRAIN 18RS21 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6816
STRAIN M732 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817
STRAIN COH1 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818
STRAIN M781 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819
STRAIN CJB110 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820
STRAIN 1169NT frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821
STRAIN JM9130013 frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822
STRAIN H36B frame: 1
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

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PRETTY of: /biotmp/msa236800.2{*}   May 14, 2003 02:58  ..

                               1                                                      50
      msa236800.2{310_090}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
    msa236800.2{310_18RS21}    ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
     msa236800.2{310_2603}     mAKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
     msa236800.2{310_A909}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
    msa236800.2{310_CJB110}    ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
     msa236800.2{310_H36B}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
  msa236800.2{310_JM9130013}   ~AKERVDVLA YKQGLFDTRE QAKRGVMAGm VINVINGERY DKPGEKVADD
     msa236800.2{310_COH1}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGl VINVINGERY DKPGEKVADD
     msa236800.2{310_M732}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGl VINVINGERY DKPGEKVADD
     msa236800.2{310_M781}     ~AKERVDVLA YKQGLFDTRE QAKRGVMAGl VINVINGERY DKPGEKVADD
    msa236800.2{310_1169NT}    ~AKERVDVLA YKQGLFDTRE QAKRGVMAGl VINVINGERY DKPGEKVADD
                Consensus      ********** ********** *********_ ********** **********

                               51                                                    100
      msa236800.2{310_090}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
    msa236800.2{310_18RS21}    TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_2603}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_A909}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
    msa236800.2{310_CJB110}    TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_H36B}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
  msa236800.2{310_JM9130013}   TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_COH1}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_M732}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
     msa236800.2{310_M781}     TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
    msa236800.2{310_1169NT}    TELKLKGEKL KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
                Consensus      ********** ********** ********** ********** **********

                               101                                                   150
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Table 68: Comparative Sequences relating to SAG 0499

```
      msa236800.2{310_090}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
    msa236800.2{310_18RS21}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_2603}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_A909}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
   msa236800.2{310_CJB110}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_H36B}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
msa236800.2{310_JM9130013}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_COH1}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_M732}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
     msa236800.2{310_M781}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
   msa236800.2{310_1169NT}  LQSGARLVYA VDVGTNQLVW KLRQDHRVRS MEQYNFRYAQ KEDFKEGLPE
                 Consensus  ********** ********** ********** ********** **********

                            151                                                200
      msa236800.2{310_090}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
   msa236800.2{310_18RS21}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_2603}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_A909}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
   msa236800.2{310_CJB110}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_H36B}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
msa236800.2{310_JM9130013}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_COH1}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_M732}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
     msa236800.2{310_M781}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
   msa236800.2{310_1169NT}  FASIDVSFIS LNLILPALKE ILVDGGQVVA LIKPQFEAGR EQIGKNGIVK
                 Consensus  ********** ********** ********** ********** **********

                            201                                                250
      msa236800.2{310_090}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
   msa236800.2{310_18RS21}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_2603}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_A909}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
   msa236800.2{310_CJB110}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_H36B}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
msa236800.2{310_JM9130013}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_COH1}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP vQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_M732}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP vQGGHGNIEF LMHLQKCQDP
     msa236800.2{310_M781}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP vQGGHGNIEF LMHLQKCQDP
   msa236800.2{310_1169NT}  DKLVHEKVLT TVTNFTKDYG YTVKHLDFSP iQGGHGNIEF LMHLQKCQDP
                 Consensus  ********** ********** ********** _********* **********

                            251                      275
      msa236800.2{310_090}  QNLVLDQIQD VIEKAHKEFK KNEEE
   msa236800.2{310_18RS21}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_2603}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_A909}  QNLVLDQIQD VIEKAHKEFK KNEEE
   msa236800.2{310_CJB110}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_H36B}  QNLVLDQIQD VIEKAHKEFK KNEEE
msa236800.2{310_JM9130013}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_COH1}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_M732}  QNLVLDQIQD VIEKAHKEFK KNEEE
     msa236800.2{310_M781}  QNLVLDQIQD VIEKAHKEFK KNEEE
   msa236800.2{310_1169NT}  QNLVLDQIQD VIEKAHKEFK KNEEE
                 Consensus  ********** ********** *****
```

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901
STRAIN 2603
ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
GTTCAAGCACAAGAAACAGATACGACGTGGACAGCACGTACTGTTTCAGAGGTAAAGGCT
GATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
GTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA
GATATCAATCTTATTTATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCAT
ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT
ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACA
ATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGACATAT
TCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA
GCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCA
GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACT
GTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCA
TCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGAC
AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCA
ACACCGGTAGCACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
GGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT
GAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC
TTTATTGTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAAT
ATGGCAGCAAATAACATTTCATATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAAC
AGTATTTATGGACCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
AACCACTATGACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTG
GCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATTA

SEQ ID NO. 6902
STRAIN 090
TGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTT
CAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCT
ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTC
TCTCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTG
TTTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAA
GTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT
ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
AGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC
GGTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTC
CTAAAGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTT
CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGA
AGTTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCGGTAG
CACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
GGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTA
TGGAGTTAATGAATTCAGTACATACCGTGCAGGTGATCCAGGTGATCATG
GTAAAGGTTTAGCAGTCGACTTTATTGTAGGTAAAAACCAAGCACTTGGT
AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTC
ATATGTTATcTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATG
GACCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
AACCATTATGACCATGTTCACGTATCATTTAACAAATAATATAAAAAAGG
AAGCTATTTGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCT
TATATAATTTTTATTA

SEQ ID NO. 6903
STRAIN A909
CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
ATATGGTGATACACTAAGCGTTATTTCAGAAGCAATGTCAATTGATATGA
ATGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCcT
GAGACAACACTGaCAGTAACTTACGATCAGAAGAGTCATACTGCTACTTC
AATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAaCAGcTA
CTGTCGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCT
CTCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGT
TTCGCCAATGAAGACATATTCTTcTGCGCCAGCTTTGAAATCAAAAGAAG
TATTAgCACAAGGGCaAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTA
TCAcCAGCTcCTGTGAAGTCGATTACTTCAGAAGTTCCAgCAGCTAAAGA
GGAAGTTAAACCAaCTCAgACGTCAgTCAGTCAGTCAACAACAGTATCAC
CAgCTTCTGTTGCCGCTGAAACACCAGCTCCAgTAGCTAAaGTAGCACCG
GTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCC
TAAAGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTC
CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA
GTTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCGGTAGC
ACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAA
GGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTAT
GGAGTTAATGAATTcAGTACATACCGTGCGGGAGATCCAGGTGATCATGG
TAAAGGTTTAGCAGTTGACTTTATTGTAgGTAAAAACCAAGCACTTGGTA
ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCaAATAACATTTCA
TATGTTATCTGGCAACAAAAGTTTTACTCAAATaCAAATAGTATTTATGG
ACcTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTAcTGCCA
ACCaCTATGACCACGTTCACGTATCATTTAACAAATaATATAAAAAAGGA
AGCTaTTTGGCTTCTTTTTTATATGCCTTGCATAGACtTTCAAGGTTCTT
ATATAATTTTTATTA

SEQ ID NO. 6904
STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA
TGGTGATACAcTAAGCGTTATTTCAGAAGCAATGTCaATTGATATGAATG
TCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCcTGAG
ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT
GAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTG
TCGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTC
AATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTC
GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTAT
TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA
CCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGA
AGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAG
CTTcTGTTGCCGCTGAAACACCAGCTCCAGTAGcTAAAGTAGCACCGGTA
AGAACTGTAGCAGCCCcTAGAGTGGCAAGTGTTAAAGTAGTCACTCcTAA
AGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTG
TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAAGTT
AAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCGGTAGCACA
ACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAAGGC
TCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGA
GTTAATGAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAA
AGGTTTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATG
AAGTTGCACAGTACTCTACACAAAAtaTGGCAGCAAATAACATTTCATAT
GTTATCTGGCaACAAAAGTTTTACTCAAATACAAATAGTATTTATGGACC
TGCTAATACTTGGAATGCAATGCCAgATCGTGGTGGCGTTACTGCCAACC
ACTATGACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGC
TATTTGGCTTCTTTTTTATATGCCTTGCATAGACtTTCAAGGTTCTTATA
TAATTTTTATTA

SEQ ID NO. 6905
STRAIN 18RS21
CTGATTTGGTAAAGCAAGACAAT
AAATCATCATATACTGTGAAATATGGTGATACAcTAAGcGTTATTTCAGA
AGCAATGTCAATTGATATGAATGTCTTAGCAAAAaTAAATAACATTGCAG
ATATCAATCTTATTTATCcTGAGACAACaCTGaCAGTAACTTACGATCAG
AAGAGTCATACTGCCaCTTCAATGAAAATAGAAACACCAGCAaCAAATGC
TGCTGGTCAaACAaCAGCTACTGTGGATTTGAAAACCAATCAaGTTTCTG
TTGCAGACCAAAAAGTTTCTCTCAATACAATTTCGGAAGGTATGACACCA
GAAGCAGCAACAACGATTGTTTCGCCAATGAAGACaTATTCTTcTGCGCC
AGCTTTGAAaTCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAG
CAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA
GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG
TCAGTCAACAACAGTATCACCAGCTTCTGTTGCCGCTGAAACACCAGCTC
CAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGCAGCCCCTAGAGTGGCA
AGTGTTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCATCACCAGAGCA
TGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGACA
GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAAGCT
CCAACAGCAACACCGGTAGCACAACCAGCTTCAACAACAAATGCAGTAGC
TGCACATCCTGAAAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAG
AAAAAGTAGCGTCAACTTATGGAGTTAATGAATTCAGTACATACCGTGCG
GGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGG
TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTcTACACAAAATA
TGGCAGCAAATAACATTTCATATGTTATCTGGCAACAAAAGTTTTACTCA
AATACAAACAGTATTTATGGACCTGCTAATACTTGGAATGCAATGCCAGA
TCGTGGTGGCGTTACTGCCAACCACTATGACCACGTTCACGTATCATTTA
ACAAATAATATAAAAAAGGAAGCTATTTGGCTTCTTTTTTATATGCCTTG
AATAGACTTTCAAGGTTCTTATATAATTTTTATTA

SEQ ID NO. 6906
STRAIN COH1
CTGATTT
GGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACAC
TAAGCGTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA
ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGAC
AGTAACTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAA
CACCAGCAACAAATGCTGCTGGTCAAACAACAGcTACTGTCGATTTGAAA
ACCAATCAAGTTTTTGTTGCAGACCAAAAAGTTTcTCTCAATACAATTTC
GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTCGCCAATGAAGA
CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAG
CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT
GAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAA
CTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTCTGTTGCC
GCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGC
AGCCCCTAGAGTGGCAAGTGcTAAAGTAGTCACTCcTAAAGTAGAAACTG
GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACT
TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC
GGTAGCACAAAAAGCTCCAACAGCAACACCGGTAGCACAACCAGCTTCAA
CAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTCAT
GTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAATT
CAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG
TTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACAG
TaCTCTACACAAAATATGGCAGCAAATAACATTTCATATGTTATCTGGCA
ACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTT
GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCAC
GTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTGGCTTC

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT
A

SEQ ID NO. 6907
STRAIN M732
CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACAnTAAGCGTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACTTACGATCAGAAGAGTCAtACTGCCACTTCAATGAAA
ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGAAAACCAATCAAGTTTTTGTTGCAGACCAAAAAGTTTCTCTCAATA
CAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCAACTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGAC
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAAGCTCCAACAGCAaCACCGGTAGCACAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTAttgtaggtaaaaaccAAGCACTTGGTAATGAAGT
TGCACAGTACTcTACACAAAATATGGCAGCAAATAACATTTCATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCT
AATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6908
STRAIN M781
CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACACTAAGCGTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTCGA
TTTGAAAACCAATCAAGTTTTTGTTGCAGACCAAAAAGTTTCTCTCAATA
CAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCAACTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGAC
TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCGGTAGCACAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGT
TGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTCATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCT
AATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTaTT
TGGCTTCTTTTTTATATGCCTTGAATAgACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6909
STRAIN CJB110
CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA
TATGGTGATACACTAAGCGTTATTTCAGAAGCAATGTCAATTGATATGAA
TGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTG
AGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTTCA
ATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCTAC
TGTGGATTTGAAAACCAATCAAGTTTcTGTTGCAGACCAAAAAGTTTCTC
TCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT
TCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGT
ATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT
CAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAG
GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC
AgCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG
TAAgAACTGTAGCAGCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT
AAAGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC
TGTGACTACGACTTCAACAGcTACAGACAGTaAGTTaCAAGCGACTGAAG
TTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCGGTAGCA
CAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG
GCTCCAACCTCATGTTGCAGCTTATaAAGAAAAAGTAGCGTCAACTTATG
GAGTTAATGAATTCAGTACATaCCGTGCAGGTGATCCAgGTGATCATGGT
AAAGGTTTAGCAGTcGACTTTATTGTAgGTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTCAT
ATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGA
CCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA
CCATTATGACCATGTTCACGTATCATTTAACAAATAATATAAAAAAGGAA
GCTATTTGGCTTCTTTTTTATATGCCTTGAATAGACtTTCAAGGTTCTTA
TATAATTTTTATTA

SEQ ID NO. 6910
STRAIN 1169NT
CTGATTTG
GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT
AAGCGTTATTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAA
TTAATAACATTGCAGATATCAATCTTATTTATCcTGAGACAACACTGACA
GTAACTTACGATCAgAAGAGTCATACTGCCACTTCAATGAAAATAGAAAC
ACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGGATTTGAAAA
CCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACAATTTCG
GAAGGTATGACACCAGAAGCAgCAACAACGATTGTTTCGCCAATGAAGAC
ATATTCTTCTGCGCCAGCTTTgAAATCAAAAGAAGTATTAGCACAAGAGC
AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG
AAGTCGATTACTTCAgAAGTTCCAgCAGCTAAAGAGGAAGTTAGACCAaC
TcAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAgCTTCTGTTGCCG
CTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGCA
GCCCCAGCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTAGA
AAcTGGTGCATCACCAGAGCATGTACCAGCTCCAGCAGTTcCTGTGACTA
cGACTTCAACAGCTACaGACAaTaAGTTACAAGCGACTGAAGTTAAgAGC
GtTCCGGTgGCACAAAAAGCTCCAACAGCAACACCGGTaGCACAACCAGC
TTcAACAACAAATGCAGTAGcTGCACATCCTGAAAATGCAGGACTCCAAC
CTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT
GAATTCAGTACATaCCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTT
AGCAGTTGACTTTATTGTagGTAAAAACCAAGCACTTGGTAATGAAGTTG
CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTCATATGTTATC
TGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA
TACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
ACCACGTTCACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTG
GCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGtTCTTATATAATTT
TTATTA

SEQ ID NO. 6911
STRAIN JM9130013
CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT
GTGAAATATGGTGATACACTAAGCGTTATTTCAGAAGCAATGTCAATTGA
TATGAATGTCTTAGCAAAAATAAATAACATTGCAGATATCAATCTTATTT
ATCcTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCC
ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAAC
AGCTACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAG
TTTCTCTCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACG
ATTGTTTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAA
AGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAAC
AGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCT
AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGT
ATCACCAgCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAG
CACCGGTAAGAACTGTAGCAGCCCCTAgAGTGGCAAGTGTTAAAGTAGTC
ACTCCTAAAGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC
AGTTCCTGTGACTACGACTTCACCAGCTACAGaCAGTAAGTTACAAGCGA
cTGAAGTTAAGAGCGTTCCGGTAGCACAAAAAGCTCCAACAGCAACACCG
GTAGCaCAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAA
TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAA
CTTATGGAGTTAATGAATTCAGTACATACCGTGCGGGAGATCCAgGTGAT
CATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACT
TGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACA
TTTCATATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAACAGTATT
TATGGACCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTAC
TGCCAACCACTATGACCACGTTCACGTATCATTTAACAAATAATATAAAA
AAGGAAGCTATTTGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGG
TTCTTATATAATTTTTATTA

```
PRETTY of: /biotmp/msa167919.2{*}   March 11, 2003 08:55  ..

                                   1                                                  50
       msa167919.2{322_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa167919.2{322_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_2603}   atgaataaaa aggtactatt gacatcgaca atggcagctt cgctattatc
  msa167919.2{322_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa167919.2{322_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa167919.2{322_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa167919.2{322_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                   Consensus   ********** ********** ********** ********** **********

                               51                                                100
```

Table 69: Comparative Sequences relating to SAG0032

```
      msa167919.2{322_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa167919.2{322_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa167919.2{322_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa167919.2{322_2603}  agtcgcaagt gttcaagcac aagaaacaga tacgacgtgg acagcacgta
  msa167919.2{322_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa167919.2{322_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa167919.2{322_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa167919.2{322_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                  Consensus  ********** ********** ********** ********** **********

                             101                                               150
      msa167919.2{322_COH1}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
      msa167919.2{322_M781}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
      msa167919.2{322_M732}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
    msa167919.2{322_18RS21}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
      msa167919.2{322_2603}  ctgtttcaga ggtaaaggct gatttggtaa agcaagacaa taaatcatca
  msa167919.2{322_JM9130013}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
       msa167919.2{322_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_CJB110}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
      msa167919.2{322_A909}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
      msa167919.2{322_H36B}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
    msa167919.2{322_1169NT}  ~~~~~~~~~~ ~~~~~~~~ct gatttggtaa agcaagacaa taaatcatca
                  Consensus  ********** ********-- ---------- ---------- ----------

                             151                                               200
      msa167919.2{322_COH1}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
      msa167919.2{322_M781}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
      msa167919.2{322_M732}  tatactgtga aatatggtga tacantaagc gttatttcag aagcaatgtc
    msa167919.2{322_18RS21}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
      msa167919.2{322_2603}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
  msa167919.2{322_JM9130013}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
       msa167919.2{322_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_CJB110}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
      msa167919.2{322_A909}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
      msa167919.2{322_H36B}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
    msa167919.2{322_1169NT}  tatactgtga aatatggtga tacactaagc gttatttcag aagcaatgtc
                  Consensus  ---------- ---------- ---------- ---------- ----------

                             201                                               250
      msa167919.2{322_COH1}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
      msa167919.2{322_M781}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
      msa167919.2{322_M732}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
    msa167919.2{322_18RS21}  aattgatatg aatgtcttag caaaaataaa taacattgca gatatcaatc
      msa167919.2{322_2603}  aattgatatg aatgtcttag caaaaataaa taacattgca gatatcaatc
  msa167919.2{322_JM9130013}  aattgatatg aatgtcttag caaaaataaa taacattgca gatatcaatc
       msa167919.2{322_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa167919.2{322_CJB110}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
      msa167919.2{322_A909}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
      msa167919.2{322_H36B}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
    msa167919.2{322_1169NT}  aattgatatg aatgtcttag caaaaattaa taacattgca gatatcaatc
                  Consensus  ---------- ---------- ---------- ---------- ----------

                             251                                               300
      msa167919.2{322_COH1}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
      msa167919.2{322_M781}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
      msa167919.2{322_M732}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
    msa167919.2{322_18RS21}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
      msa167919.2{322_2603}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
  msa167919.2{322_JM9130013}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
       msa167919.2{322_090}  ~~~~~~~~~~ TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
    msa167919.2{322_CJB110}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
      msa167919.2{322_A909}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
      msa167919.2{322_H36B}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
    msa167919.2{322_1169NT}  ttatttatcc TGAGACAACA CTGACAGTAA CTTACGATCA GAAGAGTCAT
                  Consensus  ---------- ********** ********** ********** **********

                             301                                               350
      msa167919.2{322_COH1}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
      msa167919.2{322_M781}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
      msa167919.2{322_M732}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
    msa167919.2{322_18RS21}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
      msa167919.2{322_2603}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
  msa167919.2{322_JM9130013}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
       msa167919.2{322_090}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
    msa167919.2{322_CJB110}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
      msa167919.2{322_A909}  ACTGCtACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
      msa167919.2{322_H36B}  ACTGCtACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
    msa167919.2{322_1169NT}  ACTGCcACTT CAATGAAAAT AGAAACACCA GCAACAAATG CTGCTGGTCA
                  Consensus  *****-**** ********** ********** ********** **********
```

Table 69: Comparative Sequences relating to SAG0032

```
                            351                                                400
     msa167919.2{322_COH1}  AACAaCAGCT ACTGTcGATT TGAAAACCAA TCAAGTTTtT GTTGCAGACC
     msa167919.2{322_M781}  AACAaCAGCT ACTGTcGATT TGAAAACCAA TCAAGTTTtT GTTGCAGACC
     msa167919.2{322_M732}  AACAaCAGCT ACTGTcGATT TGAAAACCAA TCAAGTTTtT GTTGCAGACC
   msa167919.2{322_18RS21}  AACAaCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
     msa167919.2{322_2603}  AACAaCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_JM9130013}  AACAaCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
      msa167919.2{322_090}  AACAcCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
   msa167919.2{322_CJB110}  AACAcCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
     msa167919.2{322_A909}  AACAaCAGCT ACTGTcGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
     msa167919.2{322_H36B}  AACAaCAGCT ACTGTcGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
   msa167919.2{322_1169NT}  AACAaCAGCT ACTGTgGATT TGAAAACCAA TCAAGTTTcT GTTGCAGACC
                 Consensus  ****-***** *****-**** ********** ********-* **********

                            401                                                450
     msa167919.2{322_COH1}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
     msa167919.2{322_M781}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
     msa167919.2{322_M732}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
   msa167919.2{322_18RS21}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
     msa167919.2{322_2603}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_JM9130013}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
      msa167919.2{322_090}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
   msa167919.2{322_CJB110}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
     msa167919.2{322_A909}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
     msa167919.2{322_H36B}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
   msa167919.2{322_1169NT}  AAAAAGTTTC TCTCAATACA ATTTCGGAAG GTATGACACC AGAAGCAGCA
                 Consensus  ********** ********** ********** ********** **********

                            451                                                500
     msa167919.2{322_COH1}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
     msa167919.2{322_M781}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
     msa167919.2{322_M732}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
   msa167919.2{322_18RS21}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
     msa167919.2{322_2603}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_JM9130013}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
      msa167919.2{322_090}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
   msa167919.2{322_CJB110}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
     msa167919.2{322_A909}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
     msa167919.2{322_H36B}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
   msa167919.2{322_1169NT}  ACAACGATTG TTTCGCCAAT GAAGACATAT TCTTCTGCGC CAGCTTTGAA
                 Consensus  ********** ********** ********** ********** **********

                            501                                                550
     msa167919.2{322_COH1}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
     msa167919.2{322_M781}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
     msa167919.2{322_M732}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
   msa167919.2{322_18RS21}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
     msa167919.2{322_2603}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_JM9130013}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
      msa167919.2{322_090}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
   msa167919.2{322_CJB110}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
     msa167919.2{322_A909}  ATCAAAAGAA GTATTAGCAC AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
     msa167919.2{322_H36B}  ATCAAAAGAA GTATTAGCAC AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
   msa167919.2{322_1169NT}  ATCAAAAGAA GTATTAGCAC AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
                 Consensus  ********** ********** ***-****** ********** *-********

                            551                                                600
     msa167919.2{322_COH1}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
     msa167919.2{322_M781}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
     msa167919.2{322_M732}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
   msa167919.2{322_18RS21}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
     msa167919.2{322_2603}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_JM9130013}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
      msa167919.2{322_090}  ATGAACAGGT ATCAaCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
   msa167919.2{322_CJB110}  ATGAACAGGT ATCAaCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
     msa167919.2{322_A909}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
     msa167919.2{322_H36B}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
   msa167919.2{322_1169NT}  ATGAACAGGT ATCAcCAGCT CCTGTGAAGT CGATTACTTC AGAAGTTCCA
                 Consensus  ********** ****-***** ********** ********** **********

                            601                                                650
     msa167919.2{322_COH1}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTtAAC
     msa167919.2{322_M781}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTtAAC
     msa167919.2{322_M732}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTtAAC
   msa167919.2{322_18RS21}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
     msa167919.2{322_2603}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_JM9130013}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
      msa167919.2{322_090}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
   msa167919.2{322_CJB110}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
     msa167919.2{322_A909}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
     msa167919.2{322_H36B}  GCAGCTAAAG AGGAAGTTAa ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
   msa167919.2{322_1169NT}  GCAGCTAAAG AGGAAGTTAg ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
                 Consensus  ********** *********- ********** ********** ******-***
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Table 69: Comparative Sequences relating to SAG0032

```
                                  651                                                700
        msa167919.2{322_COH1}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
        msa167919.2{322_M781}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
        msa167919.2{322_M732}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
      msa167919.2{322_18RS21}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
        msa167919.2{322_2603}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
   msa167919.2{322_JM9130013}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
         msa167919.2{322_090}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
      msa167919.2{322_CJB110}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
        msa167919.2{322_A909}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
        msa167919.2{322_H36B}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
      msa167919.2{322_1169NT}     AACAGTATCA CCAGCTTCTG TTGCCGCTGA AACACCAGCT CCAGTAGCTA
                    Consensus     ********** ********** ********** ********** **********

                                  701                                                750
        msa167919.2{322_COH1}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
        msa167919.2{322_M781}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
        msa167919.2{322_M732}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
      msa167919.2{322_18RS21}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
        msa167919.2{322_2603}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
   msa167919.2{322_JM9130013}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
         msa167919.2{322_090}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
      msa167919.2{322_CJB110}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
        msa167919.2{322_A909}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
        msa167919.2{322_H36B}     AAGTAGCACC GGTAAGAACT GTAG...... CAGCCCCTAG AGTGGCAAGT
      msa167919.2{322_1169NT}     AAGTAGCACC GGTAAGAACT GTAGcagccc CAGCCCCTAG AGTGGCAAGT
                    Consensus     ********** ********** ****------ ********** **********

                                  751                                                800
        msa167919.2{322_COH1}     GcTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
        msa167919.2{322_M781}     GcTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
        msa167919.2{322_M732}     GcTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
      msa167919.2{322_18RS21}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
        msa167919.2{322_2603}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
   msa167919.2{322_JM9130013}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
         msa167919.2{322_090}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
      msa167919.2{322_CJB110}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
        msa167919.2{322_A909}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
        msa167919.2{322_H36B}     GtTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
      msa167919.2{322_1169NT}     GcTAAAGTAG TCACTCCTAA AGTAGAAACT GGTGCATCAC CAGAGCATGT
                    Consensus     *-******** ********** ********** ********** **********

                                  801                                                850
        msa167919.2{322_COH1}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
        msa167919.2{322_M781}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
        msa167919.2{322_M732}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
      msa167919.2{322_18RS21}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
        msa167919.2{322_2603}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
   msa167919.2{322_JM9130013}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAcCAGCT ACAGACAgTA
         msa167919.2{322_090}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAaCAGCT ACAGACAgTA
      msa167919.2{322_CJB110}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAaCAGCT ACAGACAgTA
        msa167919.2{322_A909}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAaCAGCT ACAGACAgTA
        msa167919.2{322_H36B}     AtCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAaCAGCT ACAGACAgTA
      msa167919.2{322_1169NT}     AcCAGCTCCA GCAGTTCCTG TGACTACGAC TTCAaCAGCT ACAGACAaTA
                    Consensus     *-******** ********** ********** ****-***** *******-**

                                  851                                                900
        msa167919.2{322_COH1}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
        msa167919.2{322_M781}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
        msa167919.2{322_M732}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
      msa167919.2{322_18RS21}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
        msa167919.2{322_2603}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
   msa167919.2{322_JM9130013}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
         msa167919.2{322_090}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
      msa167919.2{322_CJB110}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
        msa167919.2{322_A909}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
        msa167919.2{322_H36B}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTaGCACA AAAAGCTCCA
      msa167919.2{322_1169NT}     AGTTACAAGC GACTGAAGTT AAGAGCGTTC CGGTgGCACA AAAAGCTCCA
                    Consensus     ********** ********** ********** ****-***** **********

                                  901                                                950
        msa167919.2{322_COH1}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
        msa167919.2{322_M781}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
        msa167919.2{322_M732}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
      msa167919.2{322_18RS21}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
        msa167919.2{322_2603}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
   msa167919.2{322_JM9130013}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
         msa167919.2{322_090}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
      msa167919.2{322_CJB110}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
        msa167919.2{322_A909}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
        msa167919.2{322_H36B}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
      msa167919.2{322_1169NT}     ACAGCAACAC CGGTAGCACA ACCAGCTTCA ACAACAAATG CAGTAGCTGC
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Table 69: Comparative Sequences relating to SAG0032

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                   Consensus  ********** ********** ********** ********** **********

                              951                                             1000
     msa167919.2{322_COH1}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
     msa167919.2{322_M781}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
     msa167919.2{322_M732}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
   msa167919.2{322_18RS21}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
     msa167919.2{322_2603}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
msa167919.2{322_JM9130013}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
      msa167919.2{322_090}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
   msa167919.2{322_CJB110}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
     msa167919.2{322_A909}    ACATCCTGAA AATGCAgGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
     msa167919.2{322_H36B}    ACATCCTGAA AATGCAaGgC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
   msa167919.2{322_1169NT}    ACATCCTGAA AATGCAgGaC TCCAACCTCA TGTTGCAGCT TATAAAGAAA
                 Consensus    ********** ******-*-* ********** ********** **********

                              1001                                            1050
     msa167919.2{322_COH1}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
     msa167919.2{322_M781}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
     msa167919.2{322_M732}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
   msa167919.2{322_18RS21}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
     msa167919.2{322_2603}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
msa167919.2{322_JM9130013}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
      msa167919.2{322_090}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCaGGt
   msa167919.2{322_CJB110}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCaGGt
     msa167919.2{322_A909}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
     msa167919.2{322_H36B}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
   msa167919.2{322_1169NT}    AAGTAGCGTC AACTTATGGA GTTAATGAAT TCAGTACATA CCGTGCgGGa
                 Consensus    ********** ********** ********** ********** ******-**-

                              1051                                            1100
     msa167919.2{322_COH1}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
     msa167919.2{322_M781}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
     msa167919.2{322_M732}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
   msa167919.2{322_18RS21}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAc
     msa167919.2{322_2603}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAc
msa167919.2{322_JM9130013}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAc
      msa167919.2{322_090}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTcGACTTTA TTGTAGGTAa
   msa167919.2{322_CJB110}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTcGACTTTA TTGTAGGTAa
     msa167919.2{322_A909}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
     msa167919.2{322_H36B}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
   msa167919.2{322_1169NT}    GATCCAGGTG ATCATGGTAA AGGTTTAGCA GTtGACTTTA TTGTAGGTAa
                 Consensus    ********** ********** ********** **-******* *********-

                              1101                                            1150
     msa167919.2{322_COH1}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
     msa167919.2{322_M781}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
     msa167919.2{322_M732}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
   msa167919.2{322_18RS21}    tAAtCAAGCA CTTGGTAATa AAGTTGCACA GTACTCTACA CAAAATATGG
     msa167919.2{322_2603}    tAAtCAAGCA CTTGGTAATa AAGTTGCACA GTACTCTACA CAAAATATGG
msa167919.2{322_JM9130013}    tAAtCAAGCA CTTGGTAATa AAGTTGCACA GTACTCTACA CAAAATATGG
      msa167919.2{322_090}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
   msa167919.2{322_CJB110}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
     msa167919.2{322_A909}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
     msa167919.2{322_H36B}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
   msa167919.2{322_1169NT}    aAAcCAAGCA CTTGGTAATg AAGTTGCACA GTACTCTACA CAAAATATGG
                 Consensus    -**-****** *********- ********** ********** **********

                              1151                                            1200
     msa167919.2{322_COH1}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAtTCAAAT
     msa167919.2{322_M781}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAtTCAAAT
     msa167919.2{322_M732}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAtTCAAAT
   msa167919.2{322_18RS21}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
     msa167919.2{322_2603}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
msa167919.2{322_JM9130013}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
      msa167919.2{322_090}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
   msa167919.2{322_CJB110}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
     msa167919.2{322_A909}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
     msa167919.2{322_H36B}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
   msa167919.2{322_1169NT}    CAGCAAATAA CATTTCATAT GTTATCTGGC AACAAAAGTT TTAcTCAAAT
                 Consensus    ********** ********** ********** ********** ***-******

                              1201                                            1250
     msa167919.2{322_COH1}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
     msa167919.2{322_M781}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
     msa167919.2{322_M732}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
   msa167919.2{322_18RS21}    ACAAAcAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
     msa167919.2{322_2603}    ACAAAcAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
msa167919.2{322_JM9130013}    ACAAAcAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
      msa167919.2{322_090}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
   msa167919.2{322_CJB110}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
     msa167919.2{322_A909}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
     msa167919.2{322_H36B}    ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
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Table 69: Comparative Sequences relating to SAG0032

```
   msa167919.2{322_1169NT}  ACAAAtAGTA TTTATGGACC TGCTAATACT TGGAATGCAA TGCCAGATCG
                 Consensus  *****-**** ********** ********** ********** **********

                            1251                                              1300
     msa167919.2{322_COH1}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
     msa167919.2{322_M781}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
     msa167919.2{322_M732}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
   msa167919.2{322_18RS21}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
     msa167919.2{322_2603}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
msa167919.2{322_JM9130013}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
      msa167919.2{322_090}  TGGTGGCGTT ACTGCCAACC AtTATGACCA tGTTCACGTA TCATTTAACA
   msa167919.2{322_CJB110}  TGGTGGCGTT ACTGCCAACC AtTATGACCA tGTTCACGTA TCATTTAACA
     msa167919.2{322_A909}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
     msa167919.2{322_H36B}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
   msa167919.2{322_1169NT}  TGGTGGCGTT ACTGCCAACC AcTATGACCA cGTTCACGTA TCATTTAACA
                 Consensus  ********** ********** *-******** -********* **********

                            1301                                              1350
     msa167919.2{322_COH1}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
     msa167919.2{322_M781}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
     msa167919.2{322_M732}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
   msa167919.2{322_18RS21}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
     msa167919.2{322_2603}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
msa167919.2{322_JM9130013}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
      msa167919.2{322_090}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
   msa167919.2{322_CJB110}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
     msa167919.2{322_A909}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGcAT
     msa167919.2{322_H36B}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGcAT
   msa167919.2{322_1169NT}  AATAATATAA AAAAGGAAGC TATTTGGCTT CTTTTTTATA TGCCTTGaAT
                 Consensus  ********** ********** ********** ********** *******-**

                            1351                             1382
     msa167919.2{322_COH1}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
     msa167919.2{322_M781}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
     msa167919.2{322_M732}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
   msa167919.2{322_18RS21}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
     msa167919.2{322_2603}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
msa167919.2{322_JM9130013}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
      msa167919.2{322_090}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
   msa167919.2{322_CJB110}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
     msa167919.2{322_A909}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
     msa167919.2{322_H36B}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
   msa167919.2{322_1169NT}  AGACTTTCAA GGTTCTTATA TAATTTTTAT TA
                 Consensus  ********** ********** ********** **
```

SEQ ID NO. 6912
STRAIN 2603 frame: 1
MNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
VISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHTATSMKIETPATNAAGQTTA
TVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTYSSAPALKSKEVLAQEQAVSQ
AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAPVAKVAPVRT
VAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVAQKAPTA
TPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD
FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6913
STRAIN 090 frame: 2
ETTLTVTYDQKSHTATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVSLNTISEGMTP
EAATTIVSPMKTYSSAPALKSKEVLAQEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVK
PTQTSVSQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSA
PAVPVTTTSTATDSKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVA
AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS
YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL
NRLSRFLYNFY

SEQ ID NO. 6914
STRAIN A909 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQGQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENARLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY

SEQ ID NO. 6915
STRAIN H36B frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQGQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENARLQPHVAAYKEKVASTYGVN

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY

SEQ ID NO. 6916
STRAIN 18RS21 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6917
STRAIN M732 frame: 3
DLVKQDNKSSYTVKYGDTXSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVFVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQVAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQLTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTASPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6918
STRAIN COH1 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVFVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQVAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQLTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6919
STRAIN M781 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVFVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQVAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQLTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6920
STRAIN CJB110 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6921
STRAIN 1169NT frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVRPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPAPRVASAKVVTPKVETGASPEHVPAPAVPVTTTSTA
TDNKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYG
VNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSN
TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6922
STRAIN JM9130013 frame: 3
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

```
PRETTY of: /biotmp/msa237049.2{*}   May 14, 2003 03:04  ..

                             1                                                50
       msa237049.2{322_COH1}  ---------- ---------- ---------- ---------- dlvkqdnkss
       msa237049.2{322_M781}  ---------- ---------- ---------- ---------- dlvkqdnkss
       msa237049.2{322_M732}  ---------- ---------- ---------- ---------- dlvkqdnkss
       msa237049.2{322_A909}  ---------- ---------- ---------- ---------- dlvkqdnkss
       msa237049.2{322_H36B}  ---------- ---------- ---------- ---------- dlvkqdnkss
        msa237049.2{322_090}  ---------- ---------- ---------- ---------- ----------
```

Table 69: Comparative Sequences relating to SAG0032

```
     msa237049.2{322_CJB110}  ---------- ---------- ---------- ---------- dlvkqdnkss
     msa237049.2{322_18RS21}  ---------- ---------- ---------- ---------- dlvkqdnkss
       msa237049.2{322_2603}  mnkkvlltst maasllsvas vqaqetdttw tartvsevka dlvkqdnkss
   msa237049.2{322_JM9130013} ---------- ---------- ---------- ---------- dlvkqdnkss
     msa237049.2{322_1169NT}  ---------- ---------- ---------- ---------- dlvkqdnkss
                   Consensus  ********** ********** ********** ********** ----------

                              51                                             100
       msa237049.2{322_COH1}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
       msa237049.2{322_M781}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
       msa237049.2{322_M732}  ytvkygdtxs viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
       msa237049.2{322_A909}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
       msa237049.2{322_H36B}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
        msa237049.2{322_090}  ---------- ---------- ---------- -------ETT LTVTYDQKSH
     msa237049.2{322_CJB110}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
     msa237049.2{322_18RS21}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
       msa237049.2{322_2603}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
   msa237049.2{322_JM9130013} ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
     msa237049.2{322_1169NT}  ytvkygdtls viseamsidm nvlakinnia dinliypETT LTVTYDQKSH
                   Consensus  ---------- ---------- ---------- -------*** **********

                              101                                            150
       msa237049.2{322_COH1}  TATSMKIETP ATNAAGQTtA TVDLKTNQVf VADQKVSLNT ISEGMTPEAA
       msa237049.2{322_M781}  TATSMKIETP ATNAAGQTtA TVDLKTNQVf VADQKVSLNT ISEGMTPEAA
       msa237049.2{322_M732}  TATSMKIETP ATNAAGQTtA TVDLKTNQVf VADQKVSLNT ISEGMTPEAA
       msa237049.2{322_A909}  TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
       msa237049.2{322_H36B}  TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
        msa237049.2{322_090}  TATSMKIETP ATNAAGQTpA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
     msa237049.2{322_CJB110}  TATSMKIETP ATNAAGQTpA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
     msa237049.2{322_18RS21}  TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
       msa237049.2{322_2603}  TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
   msa237049.2{322_JM9130013} TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
     msa237049.2{322_1169NT}  TATSMKIETP ATNAAGQTtA TVDLKTNQVs VADQKVSLNT ISEGMTPEAA
                   Consensus  ********** ********-* *********- ********** **********

                              151                                            200
       msa237049.2{322_COH1}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ vAANEQVSpA PVKSITSEVP
       msa237049.2{322_M781}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ vAANEQVSpA PVKSITSEVP
       msa237049.2{322_M732}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ vAANEQVSpA PVKSITSEVP
       msa237049.2{322_A909}  TTIVSPMKTY SSAPALKSKE VLAQgQAVSQ aAANEQVSpA PVKSITSEVP
       msa237049.2{322_H36B}  TTIVSPMKTY SSAPALKSKE VLAQgQAVSQ aAANEQVSpA PVKSITSEVP
        msa237049.2{322_090}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVStA PVKSITSEVP
     msa237049.2{322_CJB110}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVStA PVKSITSEVP
     msa237049.2{322_18RS21}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVSpA PVKSITSEVP
       msa237049.2{322_2603}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVSpA PVKSITSEVP
   msa237049.2{322_JM9130013} TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVSpA PVKSITSEVP
     msa237049.2{322_1169NT}  TTIVSPMKTY SSAPALKSKE VLAQeQAVSQ aAANEQVSpA PVKSITSEVP
                   Consensus  ********** ********** ****-***** -*******-* **********

                              201                                            250
       msa237049.2{322_COH1}  AAKEEVkPTQ TSVSQlTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
       msa237049.2{322_M781}  AAKEEVkPTQ TSVSQlTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
       msa237049.2{322_M732}  AAKEEVkPTQ TSVSQlTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
       msa237049.2{322_A909}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
       msa237049.2{322_H36B}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
        msa237049.2{322_090}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
     msa237049.2{322_CJB110}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
     msa237049.2{322_18RS21}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
       msa237049.2{322_2603}  AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
   msa237049.2{322_JM9130013} AAKEEVkPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VA..APRVAS
     msa237049.2{322_1169NT}  AAKEEVrPTQ TSVSQsTTVS PASVAAETPA PVAKVAPVRT VAapAPRVAS
                   Consensus  ******-*** *****-**** ********** ********** **--******

                              251                                            300
       msa237049.2{322_COH1}  aKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
       msa237049.2{322_M781}  aKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
       msa237049.2{322_M732}  aKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
       msa237049.2{322_A909}  vKVVTPKVET GASPEHVsAP AVPVTTTStA TDsKLQATEV KSVPVAQKAP
       msa237049.2{322_H36B}  vKVVTPKVET GASPEHVsAP AVPVTTTStA TDsKLQATEV KSVPVAQKAP
        msa237049.2{322_090}  vKVVTPKVET GASPEHVsAP AVPVTTTStA TDsKLQATEV KSVPVAQKAP
     msa237049.2{322_CJB110}  vKVVTPKVET GASPEHVsAP AVPVTTTStA TDsKLQATEV KSVPVAQKAP
     msa237049.2{322_18RS21}  vKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
       msa237049.2{322_2603}  vKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
   msa237049.2{322_JM9130013} vKVVTPKVET GASPEHVsAP AVPVTTTSpA TDsKLQATEV KSVPVAQKAP
     msa237049.2{322_1169NT}  aKVVTPKVET GASPEHVpAP AVPVTTTStA TDnKLQATEV KSVPVAQKAP
                   Consensus  -********* *******-** ********-* **-******* **********

                              301                                            350
       msa237049.2{322_COH1}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
       msa237049.2{322_M781}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
       msa237049.2{322_M732}  TAsPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
       msa237049.2{322_A909}  TAtPVAQPAS TTNAVAAHPE NArLQPHVAA YKEKVASTYG VNEFSTYRAG
       msa237049.2{322_H36B}  TAtPVAQPAS TTNAVAAHPE NArLQPHVAA YKEKVASTYG VNEFSTYRAG
```

Table 69: Comparative Sequences relating to SAG0032

```
     msa237049.2{322_090}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
  msa237049.2{322_CJB110}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
  msa237049.2{322_18RS21}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
    msa237049.2{322_2603}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
msa237049.2{322_JM9130013}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
  msa237049.2{322_1169NT}  TAtPVAQPAS TTNAVAAHPE NAgLQPHVAA YKEKVASTYG VNEFSTYRAG
                Consensus  **-******* ********** **-******* ********** **********

                           351                                                400
    msa237049.2{322_COH1}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
    msa237049.2{322_M781}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
    msa237049.2{322_M732}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
    msa237049.2{322_A909}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
    msa237049.2{322_H36B}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
     msa237049.2{322_090}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
  msa237049.2{322_CJB110}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
  msa237049.2{322_18RS21}  DPGDHGKGLA VDFIVGtNQA LGNkVAQYST QNMAANNISY VIWQQKFYSN
    msa237049.2{322_2603}  DPGDHGKGLA VDFIVGtNQA LGNkVAQYST QNMAANNISY VIWQQKFYSN
msa237049.2{322_JM9130013}  DPGDHGKGLA VDFIVGtNQA LGNkVAQYST QNMAANNISY VIWQQKFYSN
  msa237049.2{322_1169NT}  DPGDHGKGLA VDFIVGkNQA LGNeVAQYST QNMAANNISY VIWQQKFYSN
                Consensus  ********** ******-*** ***-****** ********** **********

                           401                                                450
    msa237049.2{322_COH1}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
    msa237049.2{322_M781}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
    msa237049.2{322_M732}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
    msa237049.2{322_A909}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALh
    msa237049.2{322_H36B}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALh
     msa237049.2{322_090}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
  msa237049.2{322_CJB110}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
  msa237049.2{322_18RS21}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
    msa237049.2{322_2603}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
msa237049.2{322_JM9130013}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
  msa237049.2{322_1169NT}  TNSIYGPANT WNAMPDRGGV TANHYDHVHV SFNK.YKKGS YLASFLYALn
                Consensus  ********** ********** ********** ********** *********-

                           451    460
    msa237049.2{322_COH1}  RLSRFLYNFY
    msa237049.2{322_M781}  RLSRFLYNFY
    msa237049.2{322_M732}  RLSRFLYNFY
    msa237049.2{322_A909}  RLSRFLYNFY
    msa237049.2{322_H36B}  RLSRFLYNFY
     msa237049.2{322_090}  RLSRFLYNFY
  msa237049.2{322_CJB110}  RLSRFLYNFY
  msa237049.2{322_18RS21}  RLSRFLYNFY
    msa237049.2{322_2603}  RLSRFLYNFY
msa237049.2{322_JM9130013}  RLSRFLYNFY
  msa237049.2{322_1169NT}  RLSRFLYNFY
                Consensus  **********
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Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001
STRAIN 2603

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GTGATAGAGCCTTGCTTGAGGCATTTTTATATTACCAAGCAGAGCATTTTGATGAGGAGT
GGGATAGTCTTATTCATCAGTTTATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAG
TACTTCACTTTGAGACAGATGTTTCAGCTTTTGTCCAGGCTAGTCCTTATGATACTGCTC
ATGATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACTAGATAAAC
TATCGCCGTCTGAAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAATCTGGCCACTCGTT
TTCAATTATTGGATTCCAATGGACACTACCAAACCATATCGCCGGATTCACTCTTACAAA
AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAATTTAGCGGATCGTA
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CAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGATGTAGATTTGTCTC
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GACGTAAATTTGAGATTCTAACATATTTTGACCAAATTCGAAATGAACGTTCCAAAGTCC
CAAGTTTTAGACGAGGTGATTTTGACACAGAGATGGAAATGACACCAGTCTTTGATGGCG
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CTACAGTCGAAGAAAAGGAATTAGAAAAAATTGGACAAGCCATTAGGATAGAAAATCAAG
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TTGCCTACGCCTTTTTATACCAAGAACTCAGCAGAGAAGATGCGGAGCAATTTGAAAAAG
ATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTGGAAAAGCAAGCTAGAGAAAGCTG
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